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-MODEL-frame+_n2p.model = DEV=xlp
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-Q-/cgn2_l/USPTO_Spool_VIS09899303/runat_12022003_085448_28260/app_query.fasta_1.775
-Q-/cgn2_l/USPTO_Spool_VIS09899303/runat_12022003_085448_28260/app_query.fasta_1.775
-DB-SwissProt_40 - QFMT=fastan - SUFFIX=n2p.rsp - MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cd1
-LIST=0-DCCALIGN=200 -TRA_SCORE=pct -THR_MAX=100 -THR_WIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US0989303_eCGN_1_1_19_@runat_12022003_085448_28260 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MANA -LARGEOUERY -NG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein El (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepactvirin)
(EC 3.4.21.98); Nonstructural protein NS54 (P4); Nonstructural protein NS54 (P3); Nonstructural protein NS54 (P56); Nonstructural protein NS58 (P56); Nonstructural protein NS58 (P56); Relative Control (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate Taiwan) (HCV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the
the European
                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepacivirus.
NCBI_TaxID=31645;
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SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA.
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B3AR_HUMAN
MAP4_MOUSE
B3AR_MOUSE
VE2_HPV19
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Glycoprotein; Transferase; RNA-directed RNA; Coat protein; Envelope protein; Helicase; Rerine; Protein; Hydrolase; Serine; Protein; Hydrolase; Serine; Protein; Hydrolase; Serine; Protein; Pro
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HCV_R4RP; 1.
HCV_NS4b; 1.
HCV_NS5a; 1.
HCV_NS5a; 1.
HCV_Env; 1.
HCV_env; 1.
HCV_core; 1.
HCV_core; 1.
HCV_core; 1.
HCV_CSpsid; 1.
HCV_NS3; 1.
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CORE PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

MAJOR ENVELOPE PROTEIN US2 (POTENTIAL).

NONSTRUCTURAL PROTEIN US2 (POTENTIAL).

NONSTRUCTURAL PROTEIN US4 (POTENTIAL).

NONSTRUCTURAL PROTE
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RESULT 2
POLG_HCVJ2
ID POLG_HCVJ2
AC P27959;
DT 01-AUG-1992
DT 01-AUG-1992
DT 16-OCT-2001
DE Genome poly;
DE (GP68) (GP7)
OS Hepatltis C
OC Viruses; ss;
OC Hepaclvirus
RN NCBL_TaxID=
RP SEQUENCE FR
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P27959;
P1 -AUG-1992 (Rel. 23, Last sequence update)
P1 -AUG-1992 (Rel. 23, Last sequence update)
P1 - OCT-2001 (Rel. 40, Last annotation update)
P1 - Envelope glyprotein [Contains: Capsid protein C (Core Envelope glycoprotein El (GP32) (GP35); Envelope gly (GP68) (GP70) (NS1)] (Fragment)
P1 - GP68 (GP70) (NS1)] (Fragment)
P2 - GP68 (GP70) (NS1)] (Fragment)
P3 - Hepatitis C virus (isolate HC-J2) (HCV).
P3 - GP68 (GP70) (NS1) (Fragment)
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SEQUENCE FROM N.A.
MEDLINE-92230232; PubMed-1314459;
                          NCBI_TaxID=11111;
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Tanaka T., Fukuda S.,
"Full-length sequence
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InterPro; IPR002521; HCV_core
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; PF01542; HCV_core; 1.
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;; PF01560; HCV_NS1; 1.
Dom; PD186062; HCV_NS1; 1.
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een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no rest
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requires a license agreement (See http://www.isb
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suda F., Mishiro S.;
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CAPSID PROTEIN C (POTENTIAL).
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MAJOR ENVELOPE PROTEIN E (PROMENTIAL).
MAJOR ENVELOPE PROTEIN US1 (IPOTENTIAL).
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       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein E2 (Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; NORSTRUCTURAL PROTEIN NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein NS4B (P27); Nonstructural protein NS4B (P27); Nonstructural protein NS5B (P65) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate Japanese) (ECV).

Viruses; SENNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                             Kato N., Hijikata M., Ootsuyama Y., Nakaga
Sugimura T., Shimotohno K.;
"Molecular cloning of the human hepatitis
Japanese patients with non-A, non-B hepati
Proc. Natl. Acad. Sci. U.S.A. 87:9524-9528
                                                                                                           DISCUSSION OF SEQUENCE MEDLINE-91192160; Pubme
                                                                                                                                                                                                                                                 Hepacivirus.
NCBI_TaxID=11116;
                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-91088550;
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                                                                                                                                                                                                               PubMed=2175903;
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non-B hepatitis.";
87:9524-9528(1990).
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MEROPS; S29.001; -.

MEROPS; WEROPS; WEROPS; U39.001; -.

INTERIPTO; IPR001410; DEAD.

INTERPTO; IPR002531; HCV_NS1.

INTERPTO; IPR002531; HCV_NS2.

INTERPTO; IPR002531; HCV_NS3.

INTERPTO; IPR001490; HCV_NS4.

INTERPTO; IPR002166; HCV_NS4.

INTERPTO; IPR002166; HCV_NS4.

INTERPTO; IPR002522; HCV_capsid.

INTERPTO; IPR002521; HCV_core.

INTERPTO; IPR00251; HCV_CORE.

INTERPTO; IPR00251; HCV_NS4.

INTERPTO; IPR00251; HCV_NS3.

INTERPTO; IPR00251; HCV_NS3.

INTERPTO; IPR00251; HCV_NS3.

INTERPTO; IPR00251; INTERPTO; INTERPTO; IPR00251; INTERPTO; IPR002
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InterPro;
Pfam; PFO(
Pfam; PFO(
Pfam; PFO)
Pfam; PFO
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Polyprotein; Gl
Core protein; Cl
Transmembrane;
INIT_MET
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PIR; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: THE PROTENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSITION, CYS OF THE ALL F. CATALYTIC ACTIVITY: N nucleoside tri [RNA](N).

SUBUNIT: THE VIRION OF THIS VIRUS IS LIPOPROTEIN ENVELOPE. THE ENVELOPE OF THE ENVELOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; D90208; BAA14233.1;
A39253; GNWVCJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
Coat protein
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HCV_NS4b; 1.
HCV_NS5a; 1.
HCV_NS5a; 1.
HCV_ENS; 1.
HCV_ENS; 1.
HCV_COFE; 1.
HCV_COFE; 1.
HCV_COFS; 1.
HCV_NS1; 1.
HCV_NS1; 1.
HCV_NS1; 1.
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Transferase; RNA-directed RNA polymerase;
Coat protein; Envelope protein; Helicase; ATP-binding;
Nonstructural protein; Hydrolase; Serine protease.

1 transferase; RNA-directed RNA polymerase;
CELULLAR AMINOPEPTIDASE.

115 CAPSID PROTEIN C (POTENTIAL).
191 MATRIX PROTEIN C (POTENTIAL).
192 MAJOR ENVELOPE PROTEIN MS1 (POTENTIAL).
1006 NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).
1013 NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).
1014 NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
1015 NONSTRUCTURAL PROTEIN NS4A (POTENTIAL).
1016 NONSTRUCTURAL PROTEIN NS4B (POTENTIAL).
1017 CHARGE RELAY SYSTEM (BY SIMILARITY).
1018 CHARGE RELAY SYSTEM (BY SIMILARITY).
1019 CHARGE RELAY SYSTEM (BY SIMILARITY).
1010 POTENTIAL.
1011 N-LINKED (GLCNAC. . .) (POTENTIAL).
1011 N-LINKED (GLCNAC. . .) (POTENTIAL).
1012 N-LINKED (GLCNAC. . .) (POTENTIAL).
1013 N-LINKED (GLCNAC. . .) (POTENTIAL).
1014 N-LINKED (GLCNAC. . .) (POTENTIAL).
1015 N-LINKED (GLCNAC. . .) (POTENTIAL).
1016 N-LINKED (GLCNAC. . .) (POTENTIAL).
1017 N-LINKED (GLCNAC. . .) (POTENTIAL).
1018 N-LINKED (GLCNAC. . .) (POTENTIAL).
1019 N-LINKED (GLCNAC. . .) (POTENTIAL).
1010 N-LINKED (GLCNAC. . .) (POTENTIAL).
1010 N-LINKED (GLCNAC. . .) (POTENTIAL).
1010 NOSTRUCTURAL NOTENTIAL).
1010 NONSTRUCTURAL NOTENTIAL.
1010 NONSTRUCTURAL PROTEIN NASA (POTENTIAL).
1010 NONSTRUCTURAL PROTEIN NASA (POTEN
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E. THE NUCLEOCAPSID IS A COMPLEX
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POLG_HCVJT
ID FOLG_HCVJT
AC Q00269;
DT 01-APR-1993
DT 01-APR-1993
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VITUS RES. 23:39-53(1992).

C --- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE CHYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.

C --- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

C --- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate C PROTEIN C ACTIVITY: N nucleoside triphosphate - N diphosphate C RNA)(N).

C --- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN C AND MRNA.

C --- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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MEROPS;
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Pfam;
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Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21) (EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin) (EC 3.4.21.98); Nonstructural protein NS48 (P4); Nonstructural protein NS48 (P27); Nonstructural protein NS54 (P56); Nonstructural protein NS58 (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatliis C virus (isolate HC-JT) (HCV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepaclvirus.
NCBI_TaxID-31642;
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1543; HCV_capsid; 1.
11543; HCV_capsid; 1.
11560; HCV_NS1; 1.
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Nonstructural protein;
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MAJOR ENVELOPE PROTEIN E (POTENTIAL).

MAJOR ENVELOPE PROTEIN MS1/E2 (POTENTIAL).

NONSTRUCTURAL PROTEIN MS2 (POTENTIAL).

NON-STRUCTURAL PROTEIN MS2 (POTENTIAL).

PROTEASE/HELICASE MS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN MS4A (POTENTIAL).

NONSTRUCTURAL PROTEIN MS4B (POTENTIAL).
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Love R.A., Parge H.E., Wickersham J.A., Moomaw E.W., Adachi T., Hostomska Z.; "The crystal structure of hepatitis C vitrypsin-like fold and a structural zinc cell 87:331-342(1996).
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Envelope glycoprotein E1 (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP70) (NS1); Protein P7; NS1 (P70) (Hepaclvirin)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepaclvirin)
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate EX) (HCV).

Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
  Yan Y., Li Y., Munshi S., Sardana V., Cole J.L., Sardana M.,
Steinkuehler C., Tomei L., de Francesco R., Kuo L.C., Chen Z.;
"Complex of NS3 protease and NS4A peptide of BK Strain hepatitis virus: a 2.2-A resolution structure in a hexagonal crystal form."
Protein Sci. 7:837-847(1998).
-i- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPELICATION.
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1027-1210 MEDLINE-98227846; Pubmed-9568891;
                                                                                                                                                                                                                                                                                                                         Takamizawa A., Mori C., Fuke I., Manabe S., Murakami Onishi E., Andoh T., Yoshida I., Okayama H.; "Structure and organization of the hepatitis C virus from human carriers.";
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MEDLINE=91140698; Pubmed=1847440;
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Pfam;
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PIR; #
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the European Bioinformatics Institute. The
use by non-profit institutions as modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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InterPro;
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position, Cys or Thr in P1 and Ser or Ala in E
CATALYTIC ACTIVITY: N nucleoside triphosphate
(RNA)(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1A1Q; 25-MAR-98.
1JXP; 14-JAN-98.
1NS3; 08-APR-98.
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A38465; GNWVTC
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PF02907;
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PF01001;
PF01006;
PF01506;
PF01538;
PF01542;
PF01542;
                                                                                                                                                                                                                                          201560; hcv_...3; 1.
F02907; HCV_NS3; 1.
PD186662; HCV_NS1; 1.
Ptein; Glycoprotein; Transferase; RNA-directed RNA
rotein; Coat protein; Envelope protein; Helicase; &
rotein; Coat protein; Envelope protein; Helicase; &
rotein; Coat protein; Hydroiase; Serine;
                                                                                                                                                                                                                                                                                                                                                                                                                          ; IPRO02522;
; IPRO02521;
; IPRO02519;
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| IPRO02531;
| IPRO02518;
| IPRO04109;
| IPRO04109;
| IPRO01490;
| IPRO02868;
| IPRO02166;
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112
1192
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HCV_NS4b; 1.
HCV_NS4a; 1.
HCV_NS5a; 1.
HCV_NS5; 1.
HCV_Cenv; 1.
HCV_core; 1.
HCV_Capsid;
HCV_NS1; 1.
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tdRP; 1.
fS4b; 1.
fS4a; 1.
fS4a; 1.
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HCV_NS2.
HCV_NS3.
HCV_NS4a.
HCV_NS4b.
HCV_NS5a.
HCV_RdRP.
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HCV_core.
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                                                                                                                                     CELLULAR AMINOPEPTIDASE.

CAPSID PROTEIN (C (POTENTIAL).

MATRIX PROTEIN (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1/E2 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

PROTEASE/HELICASE NS3 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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WA polymerase; ATP-binding; protease;

a

ВУ

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Pred. No.:
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RESULT 6
POLG_HCVHK
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Best Local Similarity:
Query Match:
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               GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATG
                                                           TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACAATA
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Conservative:
Mismatches:
Indels:
Gaps:
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Query Match:
DB:
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JAAO152.

JAFOTO; IPRO02531; HCV.

InterPro; IPR002531; HCV.

InterPro; IPR002522; HCV_c.

InterPro; IPR002521; HCV_c.

OR InterPro; IPR002519; HCV_env.

Pfam; PF01539; HCV_env; 1.

Pfam; PF01542; HCV_core; 1.

Pfam; PF01543; HCV_capsid; 1.

Pfam; PF01543; HCV_capsid; 1.

ODOm; PD186062; HCV_NS1; 1.

'Vprotein; Glycoprotein; Coafsmembrane; Nonstructure'

WET 1
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Q01403;
Q01403;
Q01-JUL-1993 (Rel. 26, Created)
Q01-JUL-1993 (Rel. 26, Last sequence update)
Q1-JUL-1993 (Rel. 26, Last annotation update)
Q1-Genome polyprotein [Contains: Capsid protein C (Core
Genome polyprotein [E1 (GP32) (GP35); Envelope gl;
QF058) (GP70) (NS1)] (Fragment).

Hepatitis C virus (isolate HCV-KF) (HCV).
Viruses; SRNA positive-strand viruses, no DNA stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abe K., Inchauspe G., Fujisawa K.;

"Genomic characterization and mutation rate of hepatitis C virus isolated from a patient who contracted hepatitis during an epide of non-A, non-B hepatitis in Japan.";

J. Gen. Virol. 73:2725-2729(1992).

-!- SUBBUIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED ILIPOPROTEIN ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX (PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=93019030; Abe K., Inchauspe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepacivirus.
NCBI_TaxID=31644;
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                                            CALLULAR AMINOPEPTIDASE.
CAPSID PROTEIN (POTENTIAL).
MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTEN
MAJOR ENVELOPE PROTEIN NS1/E2 (P
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTI
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         CRC64;
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

US-09-899-303A-7

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POLG_HCVHK (1-520)

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POLG_HEYNA
ID POLG_H
AC 001404
DT 01-JUL
DT 16-OUL
DT 16-OUL
DE Genome
DE Envelo
DE (GP68)
OS Hepati
OC Viruse
OC Hepati
OX NCBL_T
RN [1]
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      A Abe K., Inchauspe G., Fujisawa K.;

"Genomic characterization and mutation ra

" isolated from a patient who contracted hel

of non-A, non-B hepatitis in Japan.";

J. Gen. Virol. 73:2725-2729(1922).

-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A
LIPOPROTEIN ENVELOPE. THE ENVELOPE CON-
PROTEIN M AND GLYCOPROTEIN E. THE NUCT-
PROTEIN C AND MRNA
                                                                                                                                                                                                                                                                                                    POLG_HCVH4 STANDARD; PRT; 520 AA.

Q01404;
Q01404;
Q01404;
Q01404;
Q01-JUL-1993 (Rel. 26, Created)
Q1-JUL-1993 (Rel. 26, Last sequence update)
Q1-JUL-1993 (Rel. 26, Last sequence update)
Q1-Genome polyprotein [Contains: Capsid protein C (Coreanne polyprotein E1 (GP32) (GP35); Envelope glycoprotein E1 (GP32) (GP35); Envelope gl;
Q068) (GP70) (NS1)] (Fragment).
Hepatitis C virus (isolate HCV-476) (HCV).
Viruses; ssRNA positive-strand viruses, no DNA stagenerical contains and contains
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InterPro; IPR002531; HCV_capsid.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_env.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01543; HCV_core; 1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POT
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15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Envelope glycoprotein El (GP32) (GP35); Envelope glycoprotein E2
(GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS5A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P56) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate H) (HCV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae:
NFGT TS-1-1-1
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"Hepatitis C virus NS3 RNA helicase domain with a bound
"the crystal structure provides insights into the mode
                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
MEDLINE-98154321; PubMed-9493270;
Kim J.L., Morgenstern K.A., Griffith J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
MEDLINE=97331322; PubMed=9187654;
Yao N., Hesson T., Cable M., Hong Z.,
                                                                                                                                                                                                                                                                                             Structure 6:89-100(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nat. Struct. Biol. 4:463-467(1997).
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"Structure of the hepatitis C virus RNA
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"Genomic structure of the human
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                                             ACTIVATION OF NG3.

ACTIVATION OF NG3.

FUNCTION: NS5A SEEMS TO HAVE A TRANSCRIPTING FUNCTION: NS5B IS A RNA-DEPENDENT RNA POLY ESSENTIAL ROLE IN THE VIRUS REPLICATION.

CATALYTIC ACTIVITY: Hydrolysis of four percent of the commonly with Aspertance.
                         precursor position, CATALYTIC
                                                                                                                                                                                                 FUNCTION: PROTEASE NS2 IS RESPONSIBLE FOR THE FUNCTION: PROTEASE NS3 IS RESPONSIBLE FOR THE NS3-NS4B, NS4A-NS4B, NS4B-NS5A AND NS5A-NS5B FUNCTION: NS4A FORMS A COMPLEX WITH NS3 AND IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _HCVH
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edee S., Lee D.H.H.,
                                                                                                             SEEMS TO HAVE A TRANSCRIPTIONAL ACTIVATORY IS A RNA-DEPENDENT RNA POLYMERASE THAT PLANIN THE VIRUS REPLICATION.
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SIMILARITY: THE NS2 PROTEASE BELONGS TO PEPTIDASE FAMILY C18. SIMILARITY: THE NS3 PROTEASE BELONGS TO PEPTIDASE FAMILY S29.
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Mismatches:
Indels:
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   pfam; pF01001
pfam; pF01006;
pfam; pF01506;
pfam; pF01538;
pfam; pF01539;
pfam; pF01543;
pfam; pF01543;
pfam; pF01560;
pfam; pF02907;
Pfam; p
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HSSP; P27958; 1A1V.
MEROPS; S29.001; -.
MEROPS; U39.001; -.
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NCBI_TaxID=11104;
                                              #PTO; IPRO01410; DEAD.
#PTO; IPRO02531; HCV_NS3.
#PTO; IPRO02518; HCV_NS3.
#PTO; IPRO04109; HCV_NS3.
#PTO; IPRO04109; HCV_NS48.
#PTO; IPRO01490; HCV_NS48.
#PTO; IPRO01490; HCV_NS48.
#PTO; IPRO02868; HCV_NS48.
#PTO; IPRO02522; HCV_capsid.
#PTO; IPRO02522; HCV_capsid.
#PTO; IPRO02521; HCV_env.
#PTO; IPRO02521; HCV_env.
#PTO; IPRO02519; HCV_env.
#PTO; IPRO01650; Helicase_C; 1.
#PTO0271; helicase_C; 1.
#PTO1006; HCV_NS48; 1.
#PTO1006; HCV_NS48; 1.
#PTO1006; HCV_NS2; 1.
#PTO1548; HCV_NS2; 1.
#PTO1549; HCV_env; 1.
#PTO1549; HCV_capsid; 1.
#PTO1540; HCV_NS3; 1.
#PTO1540; HCV_NS3; 1.
#PTO1560; H
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PF00998; HCV_RdRP; 1.
PF01001; HCV_NS4a; 1.
PF01006; HCV_NS4a; 1.
PF01506; HCV_NS2; 1.
PF01538; HCV_NS2; 1.
PF01542; HCV_cenv; 1.
PF01543; HCV_cenv; 1.
PF01543; HCV_cenv; 1.
PF01560; HCV_NS1; 1.
PF01560; HCV_NS1; 1.
PF02907; HCV_NS3; 1.
Totein; Glycoprotein; Trotein; Coat protein;
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RP SEQUENCE FROM N.A.

RM MEDLINE-91172826; PUBMed-1848704;

RA Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C.,

RA Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C.,

RA Choo Q.-L., Richman K.H., Han J.H., Berger K., Lee C., Dong C.,

RA Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,

RA Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,

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RA Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,

Ra Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,

Ra Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,

"Genetic organization and diversity of the hepatitis C virus.";

"Genetic organization and diversity of the hepatitis C virus.";

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                                                                  (See http://www.isb-sib
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CAPSID PROTEIN ( POTENTIAL).

MATRIX PROTEIN ( POTENTIAL).

MAJOR ENVELOPE PROTEIN E ( POTENTIAL).

NONSTRUCTURAL PROTEIN NS1/E2 ( POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 ( POTENTIAL).

PROTEASE/HELICASE NS3 ( POTENTIAL).

NONSTRUCTURAL PROTEIN NS4A ( POTENTIAL).

NONSTRUCTURAL PROTEIN NS4B ( POTENTIAL).
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P27957;
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last sequence update)
1 16-OCT-2001 (Rel. 40, Last annotation update)
1 16-OCT-2001 (Rel. 23, Last sequence update)
1 16-OCT-2001 (Rel. 24, Last sequence update)
1 16-OCT
                                                                                                                                                 EMBL; x53134; CAA37294.1; -.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_env.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01560; HCV_NS1; 1.
ProDom; PD18602; HCV_NS1; 1.
ProDom; PD18602; HCV_NS1; 1.
Prolyprotein; Glycoprotein; Coat protein
Transmembrane; Nonstructural protein.
                                                                                                      Transmembrane;
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     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Variable and hypervariable domains are found in the regions of corresponding to the flavivirus envelope and NS1 proteins and the pestivirus envelope glycoproteins.";
Virology 180:842-848(1991).
-i- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX PROTEIN C AND MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-91112009; PubMed-1846505;

Weiner A.J., Brauer M.J., Rosenblatt
Crawford K., Bonino F., Saracco G., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=11117;
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|TrpValAlaMetThrProThrValAlaThrArgAspGlyLySLeuProAlaThrGlnLeu
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MATRIX PROTEIN (POTENTIAL).
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NSI/E2 (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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Q.-L., H
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JLG_HCVH8

D POLG_HCVH8

C P27956;

OT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Genome polyprotein [Contains: Matrix protein (Envelope protein major envelope protein E; Nonstructural protein NS1] (Fraçe Hepatitis C virus (Isolate HCT18) (HCV).

**SRNA positive-strand viruses, no DNA stage; Flagorian protein major envelope protein expression of the p
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  US-09-899-303A-7
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InterPro; IPR002531; HCV_NS1.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_env.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
Prolyprotein; Glycoprotein; Coat pr
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Virology 180:842-848(1991).
-!- SUBUNT: THE VIRION OF THIS VIRUS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the Inthe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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Pfam; PF01539; HCV_env; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01560; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
Propom; PD186062; HCV_NS1; 1.
Polyprotein; Glycoprotein; Coat protein; Entransmembrane; Nonstructural protein.
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P27955;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Genome polyprotein (Contains: Matrix protein (Envelope protein M)
Major envelope protein E; Nonstructural protein NS1] (Fragment).
Hepatitis C virus (isolate HCT27) (HCV).
Viruses; SRNA positive-strand viruses, no DNA stage; Flavivirid;
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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DIG_HCVE1 STANDARD; PRT; 192 AA.

POLG_HCVE1 STANDARD; PRT; 192 AA.

P27954;

P17954;

O1-AUG-1992 (Rel. 23, Created)

O1-AUG-1992 (Rel. 23, Last sequence update)

16-CCT-2001 (Rel. 40, Last annotation update)

Genome polyprotein [Contains: Matrix protein (E)

Major envelope protein E] (Fragment).

Hepatitis C virus (isolate EC1) (HCV).
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LL PROTEIN NSIJEZ (POTENTIAL).

CNAC. .) (POTENTIAL).
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Virology 180:842-848(1991).
-1- SUBUNIT: THE VIRION OF THIS VIRUS
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Q.-L., Houghton
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PAC. .) (POTENTIAL).
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01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Genome polyprotein [Contains: Capsid protein protein (Envelope protein M); Major envelope protein NS1 and NS2] (Fragment).
Hepatitis C virus (isolate HC-J7) (HCV).
Viruses; ssRNA positive-strand viruses, no DN
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P27961;
                                                             Pfam;
Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92230232; PubMed-1314459;
Okamoto H., Kurai K., Okada S.I., Yamamoto K., Lizuk
Tanaka T., Fukuda S., Tsuda F., Mishiro S.;
"Full-length sequence of a hepatitis C virus genome
homology to reported isolates: comparative study of
                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                  ProDom; PD186062; HCV_NS1; 1.
Polyprotein; Glycoprotein; Coat protein; Envelope protein;
                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepacivirus.
NCBI_TaxID=11114;
                        Transmembrane;
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                                                                                                                                                                                                                                                                                                    FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B AR HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRARE FELATED FUNCT NS3 AND NS5 MAY ELAY A ROLE IN THE VIRAL RNA REPLACATION. SUBUNIT: THE VIRAL OF THIS VIRUS IS A NUCLEOCAPSID COVER LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEIN PROTEIN ENVELOPENOTEIN E. THE NUCLEOCAPSID IS A COMPUPROTEIN C AND MENA.
                                                           L; D10077; BAA00971.1; -.
zrPro; IPR002531; HCV_CAPSid.
zrPro; IPR002522; HCV_core.
zrPro; IPR002521; HCV_core.
zrPro; IPR002519; HCV_env.
n; PF01543; HCV_core; 1.
n; PF01543; HCV_core; 1.
n; PF01543; HCV_CAPSid; 1.
n; PF01560; HCV_NSId; 1.
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      Nonstructural protein.

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                                    CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG
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Mismatches:
Indels:
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PROTEIN NS1/E2 (POTENTIAL).
PROTEIN NS2 (POTENTIAL).
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POLG_HCVJ8
                                   InterPro;
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InterPro;
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ro; IPR001410; ro; IPR002531; ro; IPR002518; ro; IPR004109; ro; IPR00745; ro; IPR000745; ro; IPR
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| IPR001490; | IPR002868; | IPR002166; | IPR002522; | IPR002521; | IPR002519;

DEAD.
HCV_NS1.
HCV_NS2.
HCV_NS3.
HCV_NS4a.
HCV_NS4a.
HCV_NS5a.
HCV_RdRP.
HCV_CORE1.

HCV_RdRP; 1. HCV_NS4b; 1.

GNWVJ8. 1HEI.

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genotypes.";
genotypes.";
genotypes.";
genotypes.";
yirology 188:331-341(1992).

1- FUNCTION: THE SMALL PROFISINS NS2A, NS2B, NS4A AND NS
1- FUNCTION: THE SMALL PROFISING A POSSIBLE MEMBRANE-RELATED
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICA-
1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds:
precursor polyprotein, commonly with Asp or Glu in
precursor polyprotein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Envelope glycoprotein El (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21) (EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin) (EC 3.4.21.98); Nonstructural protein NS48 (P4); Nonstructural protein NS48 (P4); Nonstructural protein NS58 (P65); Nonstructural protein NS58 (P670) (RNA-directed RNA polymerase) (EC 2.7.7.48)]. Hepatitis C virus (isolate HC-J8) (HCV).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae: Hepacivirus.
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P26661;
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MEDLINE=92230232; PubMed=1314459;

Okamoto H., Kurai K., Okada S.-I., Yama

Fukuda S., Tsuda F., Mishiro S.;

*Full-length sequence of a hepatitis C

homology to reported isolates: comparat
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01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Genome polyprotein [Contains: Capsid protein]
EMBL; D10988;
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                                                                               email to
                                                                                                                                               Bioinformatics Institute. The profit institutions as long this statement is not removed.
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PF01542;
PF01543;
PF01543;
PF01560;
PF02907;
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HCV_Env; 1.
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HCV_copsid;
HCV_NS1; 1.
HCV_NS1; 1.
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CAPSID PROTEIN C (POTENTIAL).

MAJOR ENVELOPE PROTEIN E (POTENTIAL).

NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS2 (POTENTIAL).

NONSTRUCTURAL PROTEIN NS48 (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED 
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Transferase: RNA-directed RNA polymerase;
;; Envelope protein; Helicase; ATP-binding;
:al protein; Hydrolase; Serine protease.
REMOVED FROM CAPSID PROTEIN C BY THE
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                                             GAGACGGTGCAGTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATG
                                                                      GATCTCTGCGGATCTGCCTCGTCTCCCCAGCTGTTCACCATCTCGCCTGGCCAT
                                                                                                          {\tt ArgThrHisValAspMetIleValMetAlaAlaThrAlaCysSerAlaLeuTyrValGly}
                                                                                                                      CGACGCCACGTCGATTTGCTCGTTGGGGCCGCTTTCTGTTCCGCTATGTACGTGGGG
                                                                                                                                               {\tt TrpIleGlnValThrProAsnValAlaValLysHisArgGlyAlaLeuThrArgSerLeu}
                                                                                                                                                               TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACAATA
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Search completed: February 12, 2003, 08:55:49 Job time: 27 secs

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Post-processing: Minimum Match 0%
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/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0, Version $1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION NUMBER: 32.205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION UMBER: 1487-10
TELECOMMUNICATION UMBER: 10000
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 633 base pairs
TYPE: nuclele acid
STRANDEDNESS: single
TOPOLOGY: linear
MOTIFITE TYPE: CDNA
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US-08-612-973-7
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; Sequence 7, Application US/08612973
Patent No. 6150134
GENERAL INFORMATION:
APPLICANT: MARKET
APPLICANT:
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APPLICANT: DE MARTYROFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                    MOLECULE TYPE: CL
                                                          FEATURE:
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                                                                                NAME/KEY:
LOCATION:
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LOCATION:
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US-08-324-977-11
US-08-384-616-11
US-08-904-686A-11
US-08-924-977-13
US-08-324-977-13
US-08-384-616-13
US-08-315-850-13
US-08-315-850-13
US-08-34-977-1
US-08-34-977-1
US-08-315-850-13
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Result

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Database

Minimum

Searched:

Maximum

Sequence:

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Sequence 7 Application US/08927597
Patent No 6242503
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR I
UNMBER OF SEQUENCES: 111
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US-08-927-597-7
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Best Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V.
STREET: 1100 NORTH G
                                      ADDRESSEE: NIXON
STREET: 1100 NORN
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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Similarity 100.0%;
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IBM PC compatible
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Pred. No. 1.9e-164;
                                                                                                                                               HEPATITIS C VIRUS ENVELOPE FOR DIAGNOSTIC AND THERAPEUTIC USE
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; LOCATION:
US-08-927-597-7
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FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487
TELEFONMUNICATION INFORMATION:
TELEFHONE: (703) 816-4100
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 7:
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Best Local S
Matches 633
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SOFTWARE: PATENTIN Relect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE:
CLASSIFICATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
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LOCATION:
FEATURE:
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LENGTH: 633 base pairs
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                          GGGGATCTCTGCGGATCTGTCTTCCCTGGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGG
                                                                               ATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTTCCGCTATGTACGTG
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             GGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGG
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                                                                ATACGACGCCACGTCGATTTGCTCGTTGGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTG
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CCGCTCGTCGGCGCCCCCTAGGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTT 120
                                                           TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
                                                                                                                       CTGGAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTC
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In Release #1.0, Version #1.25
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Pred. No. 1.9e-164;
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RESULT 3
US-08-612-973-13
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                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & V
                                                                                                                                                                                                                               FEATURE:
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                 61
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REFERENCE/DOCKET NUMBER: 1487-10
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TOPOLOGY: lin
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                                                                                                                                             Local
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                                                                                                                                                                                                                                                            NAME/KEY:
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                                                                                                 ATGTTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATT 60
                                                                                                                                620;
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                CCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTT
                                                                    ATGCTGGGTAAGGCCATCGATACCCTTACGTGCGGCTTCGCCGACCTCGTGGGGTACATT 60
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6150134
                                                                                                                                             Similarity
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DE MARTYNOFF, GUY
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98.1%;
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Pred. No. 6.4e-159;
0; Mismatches 12;
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Patent No. 6245503
GENERAL INFORMATION:
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APPLICANT: BUYSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR SEQUENCES: 111
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 11 MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,20
REFERENCE/DOCKET NUMBER: 1
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
Sequence 5, Application Patent No. 6150134 GENERAL INFORMATION:
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Best Local
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FEATURE:
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HYPOTHETICAL: 1
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STRANDEDNESS: single
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Pred. No. 6.4e-159;
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FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BYENE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4000
TELEFAX: (703) 816-4000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
TYPE: nucleic acid
Comparation for second
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Best Local Similarity
Matches 616; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, ve
CURRENT APPLICATION DATA:
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LOCATION:
FEATURE:
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LOCATION:
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DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE
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                                                                                                                                 APPLICATION NUMBER: US 08/612
ETLING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 795 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application Patent No. 6245503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PURIFIED HEPATITIS C VIRUS ENVELOPE TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPE
                              FEATURE:
                                             ANTI-SENSE:
                                                            MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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CITY: ARLINGTON
STATE: VIRGINIA
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 NAME/KEY:
LOCATION:
                                                                                                       STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 22201-4714
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1100 NORTH GLEBE ROAD
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DE MARTYNOFF, GUY
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US-08-927-597-5
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Best Local Similarity
Matches 616; Conserv
                                                                                                                                                                 Sequence 47, Application US/08612973 Patent No. 6150134
                                                                                                                                                        GENERAL INFORMATION:
                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                              APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED
TITLE OF INVENTION: PROTEINS
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COUNTRY:
             STATE:
                       CITY: ARLINGTON
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                                STREET:
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            VIRGINIA
                                   1100 NORTH GLEBE ROAD
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                                              NIXON & VANDERHYE P.C
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Pred. No. 8.6e-158;
0; Mismatches 12;
                                                                                 HEPATITIS C VIRUS ENVELOPE FOR DIAGNOSTIC AND THERAPEUTIC
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NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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MEDIUM TYPE: Floppy
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LOCATION:
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                                                                                                                                                                     CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG 483
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              GATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT 543
                                                                                                            GGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                                                                                Best Local Similarity Matches 613; Conserv
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GENERAL INFORMATION:
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 47,
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)815-4000
                                                                                                                                                                                                                                                                                                                           TELEFAX: (703) 816-410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pair
                                                                                                                                                                                  NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PURIFIED HEFAILLES CONTROL OF THERAPEUTIC USE TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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HYPOTHETICAL:
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CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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LOCATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
64 CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTG 123
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                         Application US/08927597
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DE MARTYNOFF, GUY
                                                                                   Conservative
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                                                                                               Score 605.8; DB 4; Pred. No. 7.7e-157;
                                                                                  Indels
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ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 NORTH GLEBE ROAD

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,973

FILING DATE: 11-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

DESCENCE TO VETT MINDER: 1187-10
                                                                                                                                                                                                                                                                                         APPLICANT: MAERTENS, GEERT
APPLICANT: BCSMAN, FONS
APPLICANT: BCSMAN, FONS
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED H
TITLE OF INVENTION: PROTEINS FO
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTTGGGATATGATGATGAACTGGT
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    INFORMATION
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                  1487-10
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RESULT 10
US-08-927-597-49
; Sequence 49, Application
; Patent No. 6245503
; GENERAL INFORMATION:
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US-08-612-973-49
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Best Local Similarity
Matches 613; Conserv
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 2433 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
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LOCATION:
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STRANDEDNESS: single
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                                                                                                 CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTG 123
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98.1%;
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Pred. No. 8e-1
0; Mismatches
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US-08-612-973-49

Patent No. GENERAL IN Sequence

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US-08-927-597-49
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Best Local Similarity
Matches 613; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
   595
                                                                                                 184
                                                                                                                                                 124 GAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTTATCTTCCTC
                                                                                                                                                                                                                                                                 355 TTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACATTCCG
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CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2433 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/927,597 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                 64 CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTTCCGGGTTCTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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               GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
                                                                                 TTGGCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTGTCCC
                                                                                                                                 GAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC
                                                                TTGGCTTTGCTGTCCTGACCGTTCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC
                                                                                                                                                                                                  CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCCTGGCGCATGGCGTCCGGGTTCTG
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BUYSE, MARIE-ANGE
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                                                                                                                                                                                                                                                                                                                                    Conservative
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98.1%;
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Pred. No. 8e-157;
0; Mismatches 12;
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; STRANDEDNESS:
; TOPOLOGY: lin:
; MOLECULE TYPE:
US-08-081-072-15
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US-08-081-072-15
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GENERAL INFORMATION:
                                                                                                                                      Matches
                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50inch, 1.4Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh Classic
SOFTWARE: Microsoft Word Version 4.0A
                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 932 base pairs
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NO. 56416540ru MAKI, Kenjiro YAMAGUCHI, Ayumi APPLICANT: TOYOSHIMA, and Michinori KOHARA
TITLE OF INVENTION: NON-A NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS
TITLE OF INVENTION: DIAGNOSIS
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CORRESPONDENCE ADDRESS:
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CITY: B
69
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                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                                                                    4 TTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCG
               CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTG 123
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CTTGTCGGCGCCCCCTAGGGGTGCTGCCAGGGCCCTGGCACATGGTGTCCGGGTTCTG
                                                                 TTGGGTAAGGTCATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGTCACCGTATG
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                                                                                                                                                    Similarity
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                                                                                                                                    Conservative
                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                       cDNA to genomic RNA
                                                                                                                                                                                                                                                        double
                                                                                                                                                                                                                                                                                                                                             435
                                                                                                                                                    88.7%;
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                                                                                                                                  Score 561.4; DB 1;
Pred. No. 8.7e-145;
0; Mismatches 41;
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                                                                                                                                    Indels
                                                                                                                                                                    Length
                                                                                                                                                                  932;
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                                                                                                                                  Gaps
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US-08-449-093A-15

: Sequence 15, Ap
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PRICE DAYS.

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/726,
APPLICATION UNMBER: 31991
TING DATE: July 8, 1991
                                                                                                                                                                                                                              ZIP: 02109-4280
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: No. 5662906oru MAKI, Kenjiro YAMAGUCHI, A)
APPLICANT: TOYOSHIMA, and Michinori KOHARA
TITLE OF INVENTION: NON-A NON-B HEPATITIS-SPECIFIC
TITLE OF INVENTION: ANTIGEN AND ITS USE IN HEPATITIS
TITLE OF INVENTION: DIAGNOSIS
                                                                                                                                               FILING DATE: May 24, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 W
CITY: Boston
STATE: Massac
COUNTRY: USA
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                                                                                                           APPLICATION NUMBER: 01 FILING DATE: June 22,
                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTGGGATATGATGATGAACTGGTAA 630
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r Street
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                                                     07/726,141
                                                                                                                08/081,072
2, 1993
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                                                                                                                                                                                                                              Patent No. 5856458
                                                                                                                                                                                                                                                  Sequence 17,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to
                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Okamoto, H
APPLICANT: Nakamura,
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                                                                                                       TITLE OF INVENTION: OLIGONUCLEOTIDE TITLE OF INVENTION: APPLICATION FOR TITLE OF INVENTION: HEPATITIS VIRUS
                                                                    NUMBER OF SEQUENCES: 3
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Pred. No. 8.
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Best Local Similarity 93.9
Matches 586; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: JP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wellacher, Robert G.
REGISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/59-47083.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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 544 GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATG
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TYPE: nucleic acid
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STATE: DC
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                                                  GATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
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                                                                                                                CGACGCCACGTCGATTTGCTCGTTGGGGCCGCTTTCTGTTCCGCTATGTACGTGGGG
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                                  GATCTCTGCGGATCTGTTTTCCTCGTCTCCCAGCTGTTCACCTTCTCGCCTCGCCGGCAT
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Pred. No. 1e-144;
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US-08-470-426B-14
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                                                                                                                                                                                                                                                                   Query Match
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APPLICANT: Okamoto, H
APPLICANT: Nakamura,
                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: JP 2-153402
PRIOR APPLICATION NUMBER: JP 2-153402
FILING DATE: 12-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weilacher, Robert G.
REBISTRATION NUMBER: 20,531
REFERENCE/DOCKET NUMBER: 06/59-47083.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 659-14
                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: unki
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,426B
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1863 base pairs
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Beveridge, ADDRESSEE: L.L.P.
                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                          GAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTC 183
                                                                                                                         CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTG 123
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                                                                                                         CTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCTTGGCACACGGTGTCCGGGTTCTG
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US-08-462-195-1
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                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/446,303

FILING DATE: 22-MAY-1995

APPLICATION NUMBER: US 08/074,584

FILING DATE: 11-JUN-1993

APPLICATION NUMBER: JP 152487/1992

FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, NO. 5789544man F.

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618
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                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHOD FOR PRODUCING TITLE OF INVENTION: HEPATITIS C VIRUS
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 416
PELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 22202
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1755 S. Jefferson Davis Highway, Suite 400
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TELEFAX: (703) 413-2220
TELEFAX: 24855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1037 base pairs
TYPE: nucleic acid
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Best Local Similarity
Matches 582; Conserv
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TOPOLOGY: lir
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                                                                                                                                        GATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
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GATCTCTGCGGATCTGTTTTCCTCATCTCCCAGCTGTTCACCTTCTCGCCTCGCCGGCAT
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                              GCTTGGGATATGATGATGAACTGGT
                                                             GAGACAGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTATCAGGCCATCGTATG
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93.1%;
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Pred. No. 2.4e-143;
 995
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Gaps

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63

Search completed: February Job time : 53 secs

18,

2003,

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

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Command line parameters:

-MODEL-frame+_n2p.model -DEV=xlp
-O-/cgn2_1/USPTO_spool/US09899303/runat_12022003_085449_28276/app_query.fasta_1.775
-DB-PIR_73 -OFMT-fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTFMT=bto -NORM-ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USER=US09899303_eCGN_1_1_48_erunat_12022003_085449_28276 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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No.
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Maximum
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ALIGNMENTS

genome polyprotein - hepatitis C virus (isolate HC-J4) (fragment)
C;Species: hepatitis C virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Nov-2000
C;Accession: PC1284
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa
Jpn. J. Exp. Med. 60, 167-177, 1990
A;Title: The 5'-terminal sequence of the hepatitis C virus genome.
A;Reference number: PC1284; MUID:91013116; PMID:2170712 Q 뫄 δÃ Вb 밁 δÃ US-09-899-303A-7 (1-633) x PC1284 (1-513) Best Local Similarity: Query Match: A;Cross-references: GB:D00832; NID:g221513; PIDN:BAA00706.1; C;Superfamily: hepatitis C virus genome polyprotein Percent Similarity: Score: Alignment Scores: A; Molecule type: genomic RNA A; Residues: 1-513 <OKA> ₹ :: 139 64 CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTTCCGGGTTCTG 123 1.63e-92 1094.00 99.52% 97.60% 94.72% Mismatches: Indels: Gaps: Length: Matches: Conservative: S.; Tanaka, T.; Yoshizawa, 513 203 4 0 0 PID:g221514 183 63 138 н.; Tsu

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C;Superfamily: hepatitis C virus
C;Keywords: polyprotein
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PN0677
hypothetical protein 787 - hepatitis C virus (fragment)
C:Species: hepatitis C virus
C:Date: 14-Jul-1994 *sequence_revision 14-Jul-1994 *text_change 17-1
C:Accession: PN0677
R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.1
Biochem. Biophys. Res. Commun. 196, 780-788, 1993
A;Title: Genomic typing of hepatitis C viruses from Korean patients.
A;Reference number: PN0677; MUID:94059104; PMID:8240354
A;Accession: PN0677
A;Molecule type: mRNA
A;Cross-references: GB:L20498; NID:91381031; PIDN:AAB02608.1; PID:91
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Bindir
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R;Chen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S.
Virology 188, 102-113, 1992
A;Title: The Taiwanese hepatitis C virus genome: sequence determination at A;Title: The Taiwanese hepatitis C virus genome: sequence determination at A;Title: The Taiwanese hepatitis C virus genome: sequence determination at A;Title: The Taiwanese hepatitis C virus genome polyprotein
A;Cccssion: A40244
A;Molecule type: genomic RNA
A;Residues: 1-3010 <CHE>
A;Cross-references: GB:M84754
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein; hydrolass
F;1-115/Product: capsid protein C #status predicted <CPC>
F;116-191/Product: envelope protein M #status predicted <CPC>
F;116-191/Product: major envelope protein B; #status predicted <NS1>
F;107-1615/Product: nonstructural protein NS2 #status predicted <NS1>
F;107-1615/Product: nonstructural protein NS2 #status predicted <NS2>
F;1310-1317/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4 #status predicted <N85>
F;196,209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,121:
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jan-2001
C;Accession: A40244
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96.15%
93.33%
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                        GNWVTW
                       (1-3010)
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A; Mclecule type: genomic RNA
A; Residues: 1-3010 <KAN's
A; Cross-references: GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:
R; Kato, N.; Ohkoshi, S.; Shimotohno, K.
Proc. Jpn. Acad. 65B, 219-223, 1989
A; Title: Japanese isolates of the non-A, non-B hepatitis viral ge
A; Reference number: PS0085
A; Accession: PS0086
A; Molecule type: genomic RNA
A; Residues: 2650-2707 <KA2>
A; Experimental source: Japanese isolate
C; Comment: The cleavage sites of this polyprotein have not been d
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-1
F; 2-115/Product: capsid protein C *status predicted <CPC>
F; 116-191/Product: envelope protein M *status predicted <EPM>
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N;Contains: capsid pro
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C;Date: 30-Jun-1992 #sequence_revision
C;Accession: A39253; PS0086
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Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990
A;Title: Molecular cloning of the human hepatitis C virus genome
A;Reference number: A39253; MUID:91088550; PMID:2175903
A;Accession: A39253
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N;Contains: capsid protein C; envelop
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C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revisio
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Matches:
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Mismatches:
Indels:
Gaps:
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n NS4b #status predicted <N4B>
n NS5 #status predicted <NS5>
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M; hepacivirin
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                                                                                         TrpValAlaLeuThrProThrLeuAlaAlaArgAsnThrSerIleProThrThrThrIle
                                                                                                   TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACAATA
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C;Accession: A45573
R;Tanaka, T.; Kato, N.; Nakagawa, M.; Ootsuyama, Y.; Cho, M.J.; Nakazawa, T.; H
Virus Res. 23, 39-53, 1992
A;Title: Molecular cloning of hepatitis C virus genome from a single Japanese c
A;Reference number: A45573
A;Status: preliminary
A;Accession: A45573; MUID:92295714; PMID:1318627
A;Accession: A45573
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-3010 <TAN>
A;Residues: 1-3010 <TAN>
A;Cross-references: GB:D11168; GB:D01171; NID:g221612; PIDN:BAA01943.1; PID:g22
A;Cross-references: GB:D1168; GB:D01171; NID:g221612; PIDN:BAA01943.1; PID:g221612; PIDN:BAA01943.1; PID
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A; restoues: 1-3010 < r/>
A; Cross-references: ExbBL:x61396; NID:g59478; PIDN:CAA43793.1; PID:g59479
A; Experimental source: isolate JK1 from an individual
R; Honda, M.; Raneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1933
Arch. Virol. 128, 163-169, 1933
A; Title: Sequence analysis of putative structural regions of hepatitis C virus isola
A; Title: Sequence analysis of putative structural regions of hepatitis C virus isola
A; Title: Sequence analysis of putative structural regions of hepatitis C virus isola
A; Title: Sequence analysis of putative structural regions of hepatitis C virus isola
A; Title: Sequence analysis of putative structural regions of hepatitis C virus isola
A; Title: Sequence extracted Road
A; Rote: this sequence is inconsistent with the nucleotide translation
A; Note: this sequence is inconsistent with the nucleotide translation
A; Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue
as Trp, and TTC for residue 771 as Ser
A; Note: the sequence extracted from NCBI backbone (NCBIN:121747, NCBIP:121748)
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; 91ycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; sf:2-115/Product: envelope protein M # status predicted <EPM>F:2-115/Product: monstructural protein NS1 status predicted <MEE>F:2-107-1615/Product: nonstructural protein NS2 status predicted <MS2>F:1015-1862/Product: nonstructural protein NS2 status predicted <NS2>F:1316-1312/Region: nucleotide-binding motif A (P-loop)
F:1311-313/Region: nucleotide-binding motif A (P-loop)
F:1316-1300/Product: nonstructural protein NS4A status predicted <N4B>F:1663-2013/Product: nonstructural protein NS5 status predicted <N4B>F:1663-2013/Product: nonstructural protein NS5 status predicted <NS5>F:1663-2013/Product: nonstructural protein NS5A status predicted <NS5>F:1663-2013/Product: nonstructural protein NS5A status predicted <NS5>F:1663-2013/Product: nonstructural protein NS5A status predicted <NS5>F:1663-2013/Product
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genome polyprotein .
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A;Variety: isolate JK1
C;Ante: 19-May-2000 #sequence_revision 19-May-2000 #text_change 23-Mar-2001
C;Ancession: S18030; S33570; A48332; S18029
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S. submitted to the EMBL Data Library, September 1991
A;Description: A whole genome of hepatitis C virus cDNA was isolated from a A;Reference number: S18028
A;Ancession: S18030
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A; Residues: 1-3010 <HON>
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC protein NS4a; nonstructural protein NS4b; nonstructural protein NS4b; nonstructural protein NS4b;
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US-09-899-303A-7
                                   Percent Similarity:
Best Local Similarity:
Query Match:
.DB;
                                                                                                                                           A; Molecule type: genomic RNA
A; Residues: 1-782 <HON>
A; Cross-references: EMBL:X61593
A; Experimental source: isolate JK2
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: capsid protein; core protein; predicted <MAT1>
F; 1-91/Product: core protein #status predicted <MAT2>
F; 384-733/Product: envelope protein #status predicted <MAT3>
F; 734-782/Product: nonstructural protein 2 (fragment) #status F
                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural
A;Reference number: S18029
A;Accession: S18031
                                                                                                                                                                                                                                                                                                                                                                   genome polyprotein - hepatit:
N;Contains: core protein; en;
C;Species: hepatitis C virus
A;Variety: isolate JK2
C;Date: 30-Jun-1992 #sequence
                                                                                                        Pred. No.:
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                                                                                                                     Alignment Scores:
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          (1-633)

    hepatitis C virus (isolate JK2) (fragment)
    rotein; envelope protein 1; nonstructural pro

                                                                                                                                                                                                                                                                                                                                         S.; Masashi, U.;
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1065.00
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94.23%
92.21%
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          (1-782)
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Conservative:
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RESULT 9

$19876

$19876

genome polyprotein - hepatitis C virus (isolate JK5) (fragment)
N;Contains: core protein; envelope protein 1; nonstructural protein
C;Species: hepatitis C virus
A;Variety: isolate JK5
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 17-N
C;Accession: $19876
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: Sequence analysis of putative structural regions of in the sequence analysis of putative structural regions of in the presence number: $18029
A;Reference number: $18029
A;Accession: $19876
A;Mclecule type: genomic RNA
A;Residues: 1-782 <HON>
A;Cross-references: EMBL:X61595; NID:g59486; PIDN:CAA43792.1; PID:g:
A;Experimental source: isolate JK5
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: capsid protein; core protein; envelope protein; glycoprof; 1191/Product: core protein #status predicted <MATI>
F;192-383/Product: envelope protein #status predicted <MATI>
F;384-733/Product: nonstructural protein 2 (fragment) #status predicted <MATI>
F;374-782/Product: nonstructural protein 2 (fragment) #status predicted <MATI>
                    Percent Similarity:
Best Local Similarit
Query Match:
DB:
                                                                        Alignment
Pred. No.:
US-09-899-303A-7
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97.60%
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Mismatches:
Indels:
                    Gaps:
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R;Bonda, M; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S. submitted to the EMBL Data Library, September 1991

A;Description: Sequence analysis of putative structural regions of la,Reference number: $18029

A;Accession: $18032

A;Molecule type: genomic RNA
A;Residues: 1-782 <HON>
A;Cross-references: EMBL:X61594
A;Experimental source: isolate JK4
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; envelope protein; glycoprof; 191/Product: core protein #status predicted <MAT1>
F;192-183/Product: envelope protein #status predicted <MAT2>
F;384-733/Product: NS1/E2 protein #status predicted <MAT3>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted
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genome polyprotein - hepatitis C virus (f N;Contains: capsid protein; envelope prote; Species: hepatitis C virus C;Date: 20-Feb-1995 #sequence_revision 19 C;Accession: S21471 R;Mogam, W.K.
submitted to the EMBL Data Library, April A;Reference number: S21471 A;Recession: S21471
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N; Takamilawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujii J. Virol. 65, 1105-1113, 1991

A; Title: Structure and organization of the hepatitis C virus genome: A; Tefference number: A38465; MUID:91140698; PMID:1847440

A; Reference number: A38465

A; Molecule type: genomic RNA

A; Residues: 1-3010 <TAK>

A; Cross·references: EMBL.M58335; NID:9329770; PIDN:AAA72945.1; PID:9: (Superfamily: hepatitis C virus genome polyprotein glycoprotein; C; Superfamily: hepatitis C virus genome polyprotein; 91ycoprotein; P:2-115/Product: capsid protein; envelope protein; hydie; 2-115/Product: major envelope protein M #status predicted <EPM>
F; 190-7389/Product: monstructural protein NS1 #status predicted <NS1>
F; 300-709/Product: nonstructural protein NS1 #status predicted <NS1>
F; 1007-1615/Product: hepacivirin #status predicted <NS2>
F; 1230-1237/Region: nucleotide-binding motif A (P-loop)
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genome polyprotein - hepatitis C virus
genome polyprotein - hepatitis C virus
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC
protein NS4a; nonstructural protein NS4b; nonstructural protein N
C;Species: hepatitis C virus
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C;Date: 31-Mar-1992 #sequence_revision
C;Accession: A38465
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polyprotein - hepatitis C virus (isolate HCV-KF)
polyprotein: C protein; E1 protein; E2/NS1 protein
C; Species: hepatitis C virus
C; Species: hepatitis C virus
C; Pate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-N
C; Accession: JQ1925
R; Abe, K.; Inchauspe, G.; Fujisawa, K.
J. Gen. Virol. 73, 2725-2729, 1992
A; Title: Genomic characterization and mutation rate of hepatitis C v
A; Reference number: JQ1925; MUID:93019030; PMID:1383400
A; Accession: JQ1925
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F;1316-1319/Region: DEXH motif
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2011/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
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RESULT 14

JH0711

genome polyprotein - hepatitis C virus (strain PRC1)
N;Contains: envelope protein E1; envelope protein E2;
C;Species: hepatitis C virus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #t.
C;Date: 17-Apr-
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A;Residues: 1-520 <ABE>
A;Residues: 1-520 <ABE>
A;Residues: 1-520 <ABE>
A;Cross references: DDBJ:D10687; NID:g221544; PIDN:BA;C;Superfamily: hepatitis C virus genome polyprotein C;Keywords: polyprotein; transmembrane protein F;1-191/Product: C protein #status predicted <CPR>
F;1-92-383/Product: E1 protein #status predicted <CPR>
F;384-520/Product: E2/NS1 protein #status predicted <I
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virus (strain PRC1)
envelope protein E2;

(fragments)
; nonstructural

protein

NS1;

#text_change

present

in

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A;Reference number: JH0711; MUID:92290283; PMID:1318245
A;Accession: JH0711
A;Molecule type: genomic RNA
A;Residues: 1-550 <LIUV
A;Cross-references: GB:M74888; GB:M74889
A;Cross-references: GB:M74888; GB:M74889
A;Note: the nucleotide sequence is not complete
A;Note: translation of the nucleotide sequence is not complete
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: envelope protein; glycoprotein; nonstructural protein; nucleocapsid; polypr
F;191-380/Product: envelope protein E2 or nonstructural protein NS1 (fragment) #status
F;381-514/Product: envelope protein E2 or nonstructural protein NS1 (fragment) #status
F;515-550/Product: nonstructural protein NS5 (fragment) #status f
F;196,233,250,305,416,422,429,447/Binding site: carbohydrate (Asn) (covalent) #status f
 RESULT 15
JQ1926
polyprotein
N;Contains:
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90.38%
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virus (isolate HCV-476)
protein; E2/NS1 protein
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A;Title: Genomic characterization and mutation rate of hepatitis (A;Reference number: JQ1925; MUID:93019030; PMID:1383400
A;Recession: JQ1926
A;Molecule type: mRNA
A;Residues: 1-523 <ABE>
A;Cross-references: DDBJ:D10687
C;Superfamily: hepatitis C virus genome polyprotein C;Superfamily: hepatitis C virus genome polyprotein F;1-191/Product: C protein #status predicted <CPR>
F;192-383/Product: E1 protein #status predicted <E1R>
F;384-523/Product: E2/NS1 protein #status predicted <E2P>
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Best Local Similarity:
Query Match:
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C;Accession: JQ1926
C;Accession: JQ1926
C;Accession: JC1926
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Search completed: February 12, 2003, 08:57:19

Job time : 36.5 secs

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-Q-/G9n2_1/USPTO_spool/US989933/runat_12022003_085450_28326/app_query.fasta_1.775
-Q-/G9n2_1/USPTO_spool/US989933/runat_12022003_085450_28326/app_query.fasta_1.775
-DB--Pending_Patents_AA_Main -OPMT-fastan -SUFETX=n2p.rapm -MINMATCH=0.1
-LOOPEL-0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST-45 -DOCALIGN=200 -THR_SCORR=-pct -THR_MXX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US09899303_CGN 1_175_Grunat_12022003_085450_28326
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MANP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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SUMMARIES

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APPLICATION NUMBER: US 08/612,973

FILING DATE: 11-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: BYRNE, THOMAS E.

REGISTRATION NUMBER: 32,205

REFERENCE/DOCKET NUMBER: 1487-10

TELEPHONE: (703) 816-4000

TELEPHONE: (703) 816-4000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,303
FILING DATE: 06-Jul-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
GACATGATCATGCACACCCCCGGGTGCGTGCGCTGCGGTTCGGGGAGAACAACTCTTCCCGG
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APPLICANT: MAERTENS, GEERT
                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 816-400
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 GGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGG
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APPLICATION NUMBER: US/08/612,973
APPLICATION NUMBER: US/08/612,973
APPLICATION NUMBER: 1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
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RESULT 3
US-09-973-025-8
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APPLICANT: MAERTI
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                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/973,025
FILING DATE: 10-Oct-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                            ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                           APPLICATION NUMBER: US 08/612, FILING DATE: 11-MAR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    TITLE OF
                                                                                                                                                                                                                                                                                                                                       GlyAspLeuCysGlySerValPheLeuValSerGlnLeuPheThrIleSerProArgArg
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STATE: VIRGINIA
                                                                                                                                                                         ADDRESSEE: NIXON & VANDERHYE P.C STREET: 1100 NORTH GLEBE ROAD
   REGISTRATION NUMBER: REFERENCE/DOCKET NUM
                                                                                                                                                  COUNTRY:
                   NAME: BYRNE,
                                                                                                                                                                                                   OF SEQUENCES:
                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                                                                         BOSMAN, FONS
DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE
INVENTION: POTEINS F
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                                                                                                                                                  U.S.A.
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                   THOMAS E
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   BER: 32,205
NUMBER: 1487-10
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US-09-995-791-8
; Sequence B, Application US/09995791
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis
; TITLE OF INVENTION: therapeutic use.
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Pred. No.:
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TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                    ATGGCTTGGGATATGATGATGACTGG 627
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; FILE REFERENCE: 2551-68
; CURRENT APPLICATION NUMBER: US/09/995,791
; CURRENT FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin 3.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-995-791-8
RESULT 5
US-09-95-808-8
; Sequence 8, Application US/09995808
; GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis C
; TITLE OF INVENTION: therapeutic use.
; FILE REFERENCE: 2551-70
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CURRENT APPLICATION NUMBER: US/09//
CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin 3.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRT
ORGANISM: Hepatitis C virus
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Sequence 8, Application US/09995860
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Purified hepatitis
TITLE OF INVENTION: therapeutic use.
FILE REFERENCE: 2551-69
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CURRENT

APPLICATION

NUMBER: US/09/995,860

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Sequence 8, Application US/10020510
(GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: purified hepatitis C vir
TITLE OF INVENTION: therapeutic use.
TITLE OF INVENTION: US/10/020,510
CURRENT APPLICATION NUMBER: US/10/020,510
CURRENT FILING DATE: 2002-07-15
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SOFTWARE: PatentIn 3.1
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Sequence 88, Application US/10128590

SEQUENCE INFORMATION:
APPLICANT: INMOGENETICS N.V.

TITLE OF INVENTION: Core-glycosylated HCV envelope
FILE REFERENCE: 135 PCT
CURRENT APPLICATION NUMBER: US/10/128,590

CURRENT FILING DATE: 2002-07-22

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PatentIn version 3.1
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#1 . 25 (EPO)

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US-09-899-303-6
; Sequence 6, Application US/09899303
; GENERAL INFORMATION:
APPLICANT: MAERIENS, GEERT
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Best Local Similarity:
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LENGTH:
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                       NUMBER OF SEQUENCES:
                                            TITLE
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                                            INVENTION:
                                                    BOSMAN, FONS
DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,20:
REFERENCE/DOCKET NUMBER: 1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                     _
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SOFTWARE: PatentIn Release #1.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,973
FILING DATE: 11-MAR-1996
                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                         GACATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAAACAACTCTTCCCGC
                                                                                                                            TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
                                                                                                                                                                                                           CTGGAAGACGGCGTGAACTATGCAACAGGGAATTTGCCCTGGTTGCTCTTTTCTCTATCTTC
           ATACGACGCCACGTCGATTTGCTCGTTGGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTG
                                                                                                               {\tt SerGlyMetTyrHisValThrAsnAspCysSerAsnSerSerIleValTyrGluAlaAla}
                               CysTrpValAlaLeuThrProThrLeuAlaAlaArgAsnAlaSerValProThrThrThr
                                                                        AspMetIleMetHisThrProGlyCysValProCysValArgGluAsnAsnSerSerArg
                                                                                                                                                                                                 {\tt LeuGluAspGlyValAsnTyrAlaThrGlyAsnLeuProGlyCysSerPheSerIlePhe}
STREET: 1100 NORTH CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
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FILING DATE: 06-Jul-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 263 amino acids
TYPE: amino acid
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TELEFAX: (703) 81
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US-09-899-303A-6
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                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                   ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ US-09-899-303A-6
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                               NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
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ATGCCTTGGGATATGATGATGAACTGG 627
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STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                          LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/899,303A FILING DATE: 06-Jul-2001 CLASSIFICATION: <Unknown>
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INVENTION: PURIFIED
PROTEINS
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DE MARTYNOFF, GUY
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1113.00
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Indels:
Gaps:
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Matches:
Conservative:
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GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
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                                                                                                          CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: UIS.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PAtentin Release #1.0, V.
CURRENT APPLICATION DATA:
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                                                     APPLICATION NUMBER: US/09/973,025
FILING DATE: 10-Oct-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON &
STREET: 1100 NORTH
           APPLICATION NUMBER: US 0
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
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RESULT 12
US-09-995-791-6
; Sequence 6, Application (
; GENERAL INFORMATION:
; APPLICANT: Innogenetics
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
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REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
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TELEFAX: (703) 81
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RESULT 13
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Sequence 6, Application C
GENERAL INFORMATION:
APPLICANT: Innogenetics
TITLE OF INVENTION: Puri
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CURRENT FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin 3.1
SEQ ID NO 6
LENGTH: 263
TYPE: PRT
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TITLE OF INVENTION: therapeutic
FILE REFERENCE: 2551-68
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TITLE F

E OF INVENTION: therapeutic use REFERENCE: 2551-70

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RESULT 14
US-09-995-860-6
; Sequence 6, Application US/09995860
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Purified hepatitis
; TITLE OF INVENTION: therapeutic use.
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CURRENT FILLING DATE: 2001-11-29
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Sequence 6, Application US/10020510 GENERAL INFORMATION:
APPLICANT: INTOGENETICS N.V.
TITLE OF INVENTION: Purified hepatitis TITLE OF INVENTION: therapeutic use.
FILE REFERENCE: 2551-72
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CURRENT FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin 3.1
SEQ ID NO 6
LENGTH: 263
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                                                                      TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
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Search completed: February Job time : 245 secs

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Minimum
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-MODEL-frame+_n2p.model -DEV=xlp
-MODEL-frame+_n2p.model -DEV=xlp
-Q-/cgr2_1/USPTO_spool/US0989303/runat_12022003_085449_28268/app_query.fasta_1.775
-Q-/cgr2_1/USPTO_spool/US0989303/runat_12022003_085449_28268/app_query.fasta_1.775
-DB-SPTREMBL_21 -QFMT-fastan -SUFFIX-n2p.rspt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN=200 -THK_SCORE-pct -THK_MAX=100 -THK_MIN=0 -ALICN=15
-MODE-LOCAL -OUTFNMT-pct -NORM-ext -HEAPSIZE-500 -MINLEN=0 -MAXLEN=2000000000
-USER-US0989303 -GCGN_1_1_88_@tunat_12022003_085449_28268 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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O49040;

O490048;

O490048;

O490040;

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InterPro; IPR00251; HCV_NS1.
Pfam; PP01542; HCV_core; 1.
Pfam; PP01539; HCV_env; 1.
Pfam; PF01539; HCV_env; 1.
Probom; Pp186062; HCV_NS1; 1.
Probom; Pp186062; HCV_NS1; 1.
Coat protein; Envelope protein; G.
Polyprotein; Transmembrane.
NON_TER 1
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081221;
01-NOV-1996
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Genome polypi
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           -1996 (TremBLrel. 01, Created)
-1996 (TremBLrel. 01, Last sequence update)
-2001 (TremBLrel. 19, Last annotation update)
polyprotein [Contains: envelope glycoprotein
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InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_NS1.
InterPro; IPR002531; HCV_NS1.
InterPro; IPR002531; HCV_NS1.
IPfam; PF01543; HCV_core; 1.
IPfam; PF01542; HCV_core; 1.
IPfam; PF0150; HCV_NS1; 1.
IPfam; PF0150; HCV_NS1; 1.
IPF0DOM; PD186062; HCV_NS1; 1.
IPF0DOM; PD186062; HCV_NS1; 1.
INTERPROTE TO THE TOTAL TO THE TOTAL
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"Nucleotide sequences of the genomic F
from a human carrier: comparison with
and divergent regions.";
J. Gen. Virol. 72:2697-2704(1991).
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NON_TER 513 513
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Mink M. Benichou
Inchauspe G.;
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Hepatitis C virus.
Viruses; ssRNA pos
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Ohba K., Homma M.
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Yoshizawa H.
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Okamoto H., Okada
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NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94270990; PubMed=7545932;
Hotta H., Doi H., Hayashi T., Pur
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5'-terminal:
J. Exp. Med.
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S., Madaule P.,
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Conservative:
Mismatches:
Indels:
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Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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Okamoto H., Kojima M., Okada S.I., Yoshizawa H., Iizuka Muchmore E.E., Peterson D.A., Ito Y., Mishiro S.;
"Genetic drift of hepatitis C virus during an 8.2-year i chimpagnzee: variability and stability.";
Virology 190:894-899(1992).
-!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PY
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IPR002522; HCV_capsid.
IPR002521; HCV_core.
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Pfam; PF01509; HCV_env; 1.

Pfam; PF01509; HCV_NS1; 1.

Pfam; PF01016; HCV_NS2; 1.

Pfam; PF010016; HCV_NS4a; 1.

Pfam; PF01001; HCV_NS4a; 1.

Pfam; PF01001; HCV_NS5a; 1.

Pfam; PF01006; HCV_NS5a; 1.

Pfam; PF010998; HCV_RS5a; 1.

Pfam; PF00998; HCV_RS1; 1.

PF0D0m; PD186062; HCV_NS1; 1.

PROSTIE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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IPR002531;
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NAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NS1 (POTENTIAL).
NON-STRUCTURAL PROTEIN NS2 (POTENTIAL).
HELICASE (NS3) (POTENTIAL).
NON-STRUCTURAL PROTEIN NS4 (POTENTIAL).
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STRAIN=RB;
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O1-NOV-1999 (TIEMBLrel. 12, C1
O1-NOV-1999 (TIEMBLrel. 21, L2
O1-JUN-2002 (TIEMBLREL. 21, L2
Genome polyprotein [Contains:
               InterPro;
InterPro;
InterPro;
InterPro;
InterPro;
InterPro;
InterPro;
  InterPro;
InterPro;
                                                                        EMBL;
HSSP;
                                                                                                                 MEDLINE-99322193; PubMed-10390360; Lohmann V., Koerner F., Koch J.O., Bartenschlager R.;
                                                                                                                                                                                                                                                                      Q9WMX2
                                                                                                                                                            Submitted
                                                                                                                                                                    Bartenschlager
                                                                                                                                                                           STRAIN-RB;
                                                                                                                                                                                               NCBI_TaxID=31647;
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                                                                  MEROPS;
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                                                                                                           Replication
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                                                                               ence 285:110-113(1999).
SIMILARITY: TO HEPATITIS
L; AJ238799; CAB46677.1;
                                                                                                                                                                                                                                                                                                                            GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCCGGCCACATAACAGGTCACCGTATG
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                                                                        AJ238799;
P26663; 1:
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                      IPR002522;
IPR002521;
IPR002519;
IPR002531;
IPR002518;
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1 (MAY-1999)
  IPR004109;
IPR000745;
IPR001490;
                                                          29.001; -.
IPR001410;
                                                                                                                                                                                                            virus type 1b.
RNA positive-strand
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HCV_capsid.
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HCV_NS1.
HCV_NS3.
HCV_NS4.
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Best Local Similarity:
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InterPro; IPR002166; HCV_RdRP.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01539; HCV_env; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01538; HCV_NS2; 1.
Pfam; PF01538; HCV_NS3; 1.
Pfam; PF01006; HCV_NS3; 1.
Pfam; PF01001; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF01506; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
ProDom; PD186062; HCV_NS1; 1.
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'y Match:
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ATGATCATGCACACCCCCGGGTGCGTGCGCTTCGGGAGAAAAACTCTTCCCGGTGC
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GLYCOPROTEIN E1.
GLYCOPROTEIN E2.
P7 PROTEIN.
NS2 PROTEINASE.
NS3 PROTEINASE/HELICASE.
NS3/AA PROTEINASE COFACTO
NS4B PROTEIN.
NS5A PHOSPHOPROTEIN.
NS5A PHOSPHOPROTEIN.
NS5A PHOSPHOPROTEIN.
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3 RNA DEPENDANT RN
37B3448DAFA9A10B
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RNA-directed RNA polymerase;
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258

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Best Local Similarity:
Query Match:
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              US-09-899-303A-7 (1-633) x Q9J3H2
                                                   Percent Similarity:
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Polyprotein; RNA-di
SEQUENCE 3010 AA;
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01-OCT-2000
01-JUN-2002
                                                                                                                                   Pfam;
Pfam;
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Pfam;
Pfam;
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HSSP;
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MEROPS; U39
                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-1999)
                                                                                                                                                                                                                                                                                                                                         progression."
                                                                                                                                                                                                                                                                                                                                              Nagayama K., Kurosaki M., Enomoto N., "Characteristics of hepatitis C viral
                                                                                                                                                                                                                                                                                                                                                               STRAIN-MD20;
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                                                                                                                                                                                                                                                                                                                                                                                             Hepacivirus
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L; AF207761; AAF
P; P26663; 1NS3.
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PF01539;
PF01560;
PF01538;
PF02907;
PF01006;
TTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCG
                                                                                                                            PF01506;
PF00998;
                                                                                                                                                                                                                                                                                                                                                                                                                        polyprotein
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IPRO01410;
IPRO02521;
IPRO02521;
IPRO02519;
IPRO02518;
IPRO02518;
IPRO04109;
IPRO04109;
IPRO01490;
IPRO002868;
                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
protein (Contains: envelope glycoprotein
                                                                                              0190; CYTOCHROME_C;
; Envelope protein;
RNA-directed RNA po
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                          HCV_capsid; 1
HCV_core; 1.
HCV_env; 1.
HCV_env; 1.
HCV_NS1; 1.
HCV_NS2; 1.
HCV_NS3; 1.
HCV_NS4a; 1.
HCV_NS4a; 1.
HCV_NS4a; 1.
HCV_NS5a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                   positive-strand
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                                                                                                                     HCV_NS1;
                             7.83e-97
1091.00
99.04%
96.63%
94.46%
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HCV_core.
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HCV_NS2.
HCV_NS3.
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                                                                                        MW;
              (1-3010)
                                                                                              C; UNKNOWN_1.
n; Glycoprotein; Nonstructural
polymerase; Transmembrane.
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                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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      Roch J O., Bartenschlager R.;
Modulation of hepatitis C virus NS
nonstructural proteins NS3, NS4A, a
J. Virol. 73:7138-7146(1999)
.-- SIMILARITY: TO HEPATITIS C VIRUEMBL; AV338800; CAB53095.1; -.
HSSP; P26663; INS3.
                                                                                                                                                                       01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                      Bartenschlager R.;
Submitted (MAY-1999)
                                                                                                                           Hepacivirus.
NCBI_TaxID=31647;
                                                                                                                                         Viruses; ssRNA
                                                                                                                                                                                                      09QP06
                                                         MEDLINE=99370154; PubMed=10438800
                                                                  STRAIN-RB;
                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                         positive-strand
                                                                                                                                                 type
                                                                                                                                                                [Contains:
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                     VIRUS
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303 198 243 183 158 123 138

238

E2

(GP68) (GP70)

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IPR001410; IPR0025

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ATP-binding;
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                                                                                                                                                         TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACAATA
                                          Scores:
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    PF01543; HC
    PF01539; HC
    PF01538; HC
    PF01538; HC
    PF01538; HC
    PF01506; HC
    PF01006; HC
    PF01506; HC
    PF01998; HC
               {\tt MetIleMetHisThrProGlyCysValProCysValArgGluAsnAsnSerSerArgCys}
                     ATGATCATGCACACCCCCGGGTGCCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC
                                                                                                                 GAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTC
                                                                                                                                                                                                                 Similarity:
                                                                                                                                                                                                                                                                                                                                                           PD186062;
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                                                                                                                                                                                                                                                           384
747
747
810
1027
1658
1712
1973
2419
3010
                                                                                                                                                                                                                                                                                                                                                    Coat
                                                                                                                                                                                                                                                                                                                                            062; HCV_NS1; 1.
Coat protein; Envelope protein; Polyprotein;
                                                                                                                                                                                                                                                                                                                                                                HCV_caps1d; 1
HCV_core; 1.
HCV_env; 1.
HCV_env; 1.
HCV_NS1; 1.
HCV_NS3; 1.
HCV_NS4a; 1.
HCV_NS4b; 1.
HCV_NS4b; 1.
HCV_NS4b; 1.
HCV_NS4b; 1.
                                                                                                                                                                                                                                                           AA;
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383
746
809
1026
1657
1711
1972
2418
3010
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1090.00
99.04%
96.63%
94.37%
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HCV_core.
HCV_env
HCV_NS1.
HCV_NS3.
HCV_NS4.
HCV_NS48.
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HCV_RdRP.
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                                                                                                                                                                                                                                                                                                           CORE PROTEIN.
GLYCOPROTEIN GLYCOPROTEIN P7 PEPTIDE.
                                                                                                                                                                                      (1-3010)
                                                                                                                                                                                                                                                                       NS2 PROTEINASE.

NS3 PROTEINASE/HELICASE.

NS3/4A PROTEINASE COFACTOR.

NS4B PROTEIN.

NS5A PHOSPHOPROTEIN.
                                                                                                                                                                                                                                                         NA DEPENDANT RNA POLYMERASE. A570BB980DD64634 CRC64;
                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                             protein; Gly
RNA-directed
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R Interpro; IPROUISO; Helicase_C.

R Pfam; PF01543; HCV_core; 1.

R Pfam; PF01542; HCV_core; 1.

R Pfam; PF01539; HCV_MS1; 1.

R Pfam; PF01539; HCV_MS2; 1.

R Pfam; PF01006; HCV_MS3; 1.

R Pfam; PF01006; HCV_MS4a; 1.

R Pfam; PF01001; HCV_MS4a; 1.

R Pfam; PF01001; HCV_MS4a; 1.

R Pfam; PF01001; HCV_MS5a; 1.

R Pfam; PF010021; helicase_C; 1.

R Pfam; PF00271; helicase_C; 1.

R PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

W Coat protein; Envelope protein; Glycoprotein; Nonstructural pro Polyprotein; RNA-directed RNA polymerase; Transmembrane.

O SEQUENCE 3010 AA; 326692 MW; 074098DB305AF1A9 CRC64;
                                                                                                                                               Interpro;
Interpro;
Interpro;
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Interpro;
Interpro;
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InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                  progression.;
Submitted (NOV-1999) to the
-1- SIMILARITY: TO HEPATITIS
EMBL; AF207753; AAF65943.1;
HSSP; P26663; JJXP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9J3I0;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Cr
01-OCT-2000 (TrEMBLrel. 15, La
01-JUN-2002 (TrEMBLrel. 21, La
Genome polyprotein [Contains:
                                                                                                                                                                                                                                                                 MEROPS; S29.001;
MEROPS; U39.001;
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                                                                                                                                                                                                                                                                                                                                        Nagayama K.,
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                   Hepacivirus
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hepatitis C viral
                                                                                                                                                       HCV_capsid.
HCV_core.
HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS3.
HCV_NS4a.
HCV_NS4b.
HCV_RGRP.
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15, Last sequence update)
21, Last annotation update)
tains: envelope glycoprotein
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S C VIRUS ENVELOPE
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GLYCOPROTEIN
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                                                                      Genome polyprotein [Contains: en (NSI)].
Hepatitis C virus.
Viruses; ssRNA positive-strand v Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                             Q9J3G7
Q9J3G7;
Q9J3G7;
Q1-OCT-2000
Q1-OCT-2000
Q1-JUN-2002
  Nagayama K., Kurosaki M., 
"Characteristics of hepat 
progression.";
                                   STRAIN-MD25;
                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                           484
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
protein [Contains: envelope glycoprotein
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                                                 N.A.
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1089.00
98.08%
96.63%
94.29%
           ki M., Enomoto N.,
hepatitis C viral
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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           Miyasaka Y., Marun
genome associated
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disease
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Pred. No.:
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CC -1 - SIMILARITY: TO THE EMPLY DELIBERTY DELIBERTY FOR THE PROPERTY OF THE P
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Indels:
Gaps:
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GLYCOPROTEIN
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Q9QIY3; Q1-MAY-2000 (TrEMBLrel. 13, Created of the contains of the contain
                        Pfam; P
ProDom;
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Pfam;
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Pfam;
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InterPro;
InterPro;
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InterPro;
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InterPro;
InterPro;
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-!- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis
Viruses; s
                                                                        Pfam;
                                                                                           Pfam;
                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20013325; PubMed=10544098;
Nagayama K., Kurosaki M., Enomoto N., Maekawa S
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MD4-2;
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ro; IPRO01410; DEAD.
ro; IPRO01410; DEAD.
ro; IPRO02521; HCV_copsid.
ro; IPRO02521; HCV_core.
ro; IPRO02521; HCV_NS1.
Pro; IPRO02518; HCV_NS1.
Pro; IPRO02518; HCV_NS3.
rPro; IPRO04109; HCV_NS4a.
rPro; IPRO004109; HCV_NS4b.
rPro; IPRO01490; HCV_NS4b.
rPro; IPRO02166; HCV_NS4b.
rPro; IPRO02166; HCV_RS5a.
arPro; IPRO02166; HCV_RS1; 1.
m; PF01543; HCV_core; 1.
m; PF01543; HCV_core; 1.
m; PF01539; HCV_NS1; 1.
am; PF01539; HCV_NS1; 1.
am; PF01506; HCV_NS1; 1.
fam; PF01006; HCV_NS3; 1.
fam; PF01006; HCV_NS4a; 1.
fam; PF01006; HCV_NS4a; 1.
fam; PF01006; HCV_NS4a; 1.
fam; PF01001; HCV_NS4a; 1.
fam; PF01006; HCV_NS4a; 1.
fam; PF01006; HCV_NS4a; 1.
fam; PF01001; HCV_NS4a; 1.
fam; PF01001; HCV_NS4a; 1.
fam; PF01001; HCV_NS4a; 1.
      ATP-binding;
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no F., Sato C.
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Percent Similarity:
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Pred. No.:
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                                Q81760 PRELIMI
Q81760;
01-NOV-1996 (TIEMBL:
01-NOV-1996 (TIEMBL:
01-JUN-2002 (TIEMBL:
Genome polyprotein
         Hepatitis
Viruses; s
                        (NS1)]
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SEQUENCE 3010 AA; 327087 MW; 2FF78321686D4002 CRC64;
Hepacivirus
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        SSRNA
                 C virus
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(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 21, Last annotation update)
protein [Contains: envelope glycoprotein
                                                                              PRELIMINARY;
       positive-strand
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1086.00
99.04%
96.15%
94.03%
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       viruses,
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Matches:
Conservative:
Mismatches:
Indels:
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InterPro;
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ATP-binding; Coat protein;
Nonstructural protein; Poly
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ATP-binding; Coat
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MEROPS; U39.001;
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"Prevalence, Genotypes, and an Isolate(HC-C2)
Chinese Patients With Liver Disease.";
J. Med. Virol. 40:254-260(1993).
                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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            PF01543;
PF01542;
PF01539;
PF01538;
PF01006;
PF01001;
PF01001;
PF01506;
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IPR00252
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HCV_env; 1
HCV_env; 1
HCV_env; 1
HCV_NS1; 1
HCV_NS2; 1
HCV_NS3; 1
HCV_NS4b; 1
HCV_NS5a; 1
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97.60%
97.12%
94.03%
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HCV_NS1.
HCV_NS2.
HCV_NS3.
HCV_NS4a.
HCV_NS4b.
HCV_NS4b.
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HCV_capsid
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tein; Envelope |
; Polyprotein; |
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Matches:
Conservative:
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Indels:
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RNA-directed
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2) of
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                                    pfam: pF01539; HCV_env; 1.
pfam: pF01530; HCV_NSI; 1.
pfam: pF01538; HCV_NS2; 1.
pfam: pF01538; HCV_NS2; 1.
pfam: pF01006; HCV_NS4a; 1.
pfam: pF01001; HCV_NS4b; 1.
pfam: pF01906; HCV_NS5a; 1.
pfam: pF019098; HCV_NS5a; 1.
pfam: pF00998; HCV_NS1; 1.
pfam: pF018602; HCV_NS1; 1.
probom: pD18602; HCV_NS1; 1.
ATP-binding: Coat protein; En'
Nonstructural protein; Polypro
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01-NOV-1998
01-NOV-1998
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                                                                                                                          Pfam,
Pfam,
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Pfam,
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Viruses; ssRNA positive-strand
Hepaclvirus.
NCBI_TaxID=11103;
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MEROPS; U39.001;
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(TrEMBLrel.)
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HCV_env.
HCV_NS1.
HCV_NS2.
HCV_NS3.
HCV_NS4a.
HCV_NS4a.
HCV_NS5a.
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cein; Envelope
Polyprotein;
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RNA-directed RNA polymerase;
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Pred. No.
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Q9QIY4;
Q9QIY4;
Q1-MAY-2000 (TREMBLrel. 13, Crea'
01-MAY-2000 (TREMBLrel. 13, Last
01-JUN-2002 (TREMBLrel. 21, Last
          Nagayama
Tazawa J.
                                 STRAIN=MD4-1;
MEDLINE=20013325; PubMed=10544098;
                                                           SEQUENCE FROM
                                                                                                    Viruses;
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NCBI_TaxID=11103;
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           Kurosaki M., Enomoto
Izumi N., Marumo F.,
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InterPro; IPR00252; HCV_capsid.

InterPro; IPR002521; HCV_env.

InterPro; IPR002513; HCV_NS1.

InterPro; IPR002513; HCV_NS1.

InterPro; IPR002518; HCV_NS3.

InterPro; IPR0001409; HCV_NS3.

InterPro; IPR0001490; HCV_NS4A.

InterPro; IPR001490; HCV_NS4A.

InterPro; IPR001490; HCV_NS4A.

InterPro; IPR002166; HCV_RdRP.

InterPro; IPR002166; HCV_RdRP.

InterPro; IPR002166; HCV_RdRP.

IPfam; PF01543; HCV_capsid; 1.

Pfam; PF01543; HCV_capsid; 1.

Pfam; PF01549; HCV_NS1; 1.

Pfam; PF01549; HCV_NS1; 1.

Pfam; PF01506; HCV_NS4a; 1.

Pfam; PF01006; HCV_NS5a; 1.

Pfam; PF0
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EMBL; AF165051; AAD56186.1;
HSSP; P26663; LJXP.
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-!- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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-1- SIMILARITY: TO HEPATITIS C VIRUS ENBL; D00574; BAA00452.1; ...
InterPro; IPR002522; HCV_core.
InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_MS1.
InterPro; IPR002531; HCV_MS1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_mS1; 1.
Pfam; PF01549; HCV_MS1; 1.
Pfam; PF01560; HCV_MS1; 1.
                                                                                                                                                                                  STRAIN-HJJAPAN/J1 AND JH/JAPAN/J1;
STRAIN-HJJAPAN/J1 AND JH/JAPAN/J1;
MEDLINE-90356432; PubMed-2117749;
Takeuchi K., Kubo Y., Boonmar S., Watanabe Y., Katayama Kuo G., Houghton M., Saito I., Miyamura T.;
"Nuclectide sequence of core and envelope genes of the hvirus genome derived directly from human healthy carrier Nucleic Acids Res. 18:4626-4626(1990).
                                                                                                                                                                                                                                                               SEQUENCE OF 325-441 FROM N.A.

STRAIN-JH/JAPAN/J7 AND JH/JAPAN/J1;

MEDLINE-91007289; PubMed-2170237;

Takeuchi K., Boonmar S., Kubo Y., Katayama T., Harada H.,

Ohbayashi A., Choo Q., Kuo G., Houghton M., Saito I., Miyamura

"Hepatitis C viral cDNA clones isolated from a healthy carrier

implicated in post-transfusion non-A, non-B hepatitis.";

Gene 91:287-291(1990).
                                                                                                                                                                                                                                                                                                                                                                                              Genome
(NS1)
                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-JH/JAPAN/J7 AND JH/
MEDLINE-94270990; PubMed-7
Hotta H., Doi H., Hayashi
                                                                                                                                                                                                                                                                                                                                                         Hepacivirus.
NCBI_TaxID=11103;
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01-DEC-2001
                                                                                                                                                                      SEQUENCE FROM N
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                                                                                                      Arch.
                                                                                                               variant
                                                                                                                        *Analysis of the core and El
                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus.
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                                                                                                                                  K., Homma
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                                                                                                                                                                                                                                                                                                                                                                                              polyprotein
(Fragment).
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
protein [Contains: envelope glycoprotein
                                                                                                                                        JH/JAPAN/J1;
ed=7545932;
shi T., Purwanta
                                                                                                              and El envelope
virus obtained
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                                                                                             ENVELOPE
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in Indonesia.";
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                       Q68520 PRELIMINARY; PI
Q68520; O1-NOV-1996 (TrEMBLrel. 01, Cree
01-NOV-1996 (TrEMBLrel. 19, Las:
01-DEC-2001 (TrEMBLrel. 19, Las:
Genome polyprotein [Contains: e
(NS1)] (Fragment).
Hepatitis C virus.
Viruses; SERNA positive-strand
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NON TER 441 441
SEQUENCE 441 AA; 47875 MW;
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1084.00
98.56%
95.67%
93.85%
                             strand
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                                                                                                    PRT;
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                            viruses,
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78025F07957EF41E
                                      Glycoprotein;
                                       Nonstructural
                                       protein;
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGGTCCGGGTTCTG

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303 198 243

363 218

TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACATA

423

238

TrpValAlaLeuThrProThrLeuAlaAlaArgAsnAlaSerValProThrThrThrLeu

543 278 483 258

GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCCGGCCACATAACAGGTCACCGTATG

318 603

Created)
Last sequence update)
Last annotation update)
s: envelope glycoprotein A

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InterPro; IPR002521; HCV_core.
InterPro; IPR002521; HCV_sore.
InterPro; IPR002531; HCV_NS1.
InterPro; IPR002531; HCV_NS2.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
Pfam; PF01543; HCV_core; 1.
Pfam; PF01569; HCV_NS1; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF01560; HCV_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM STRAIN-HTX; Mueller H.M.,
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NON_TER 802 802
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"Recurrent hepatitis C virus infection after liver transpl
a patient negative for viral proteins: A possible role of
        544
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       GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATG
                      TrpValAlaLeuThrProThrLeuAlaAlaArgSerAlaAsnValSerThrThrThrIle
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S; U39.001; -.
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S C VIRUS ENVELOPE
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Matches:
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GLYCOPROTEIN
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InterPro; IPR001410; DEAD.
InterPro; IPR002522; HCV_cops1d.
InterPro; IPR002531; HCV_core.
InterPro; IPR002531; HCV_sor.
InterPro; IPR002531; HCV_NS2.
InterPro; IPR002531; HCV_NS3.
InterPro; IPR002531; HCV_NS3.
InterPro; IPR000745; HCV_NS4A.
InterPro; IPR001400; HCV_NS4A.
InterPro; IPR001400; HCV_NS5A.
InterPro; IPR001266; HCV_NS5A.
InterPro; IPR002166; HCV_RdRP.
Pfam; PF01543; HCV_caps1d; 1.
Pfam; PF01542; HCV_caps1d; 1.
Pfam; PF01539; HCV_NS1; 1.
Pfam; PF01539; HCV_NS2; 1.
Pfam; PF01539; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS4b; 1.
PF0000m; PD186062; HCV_NS4b; 1.
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                                                                                                                                                          Coat protein; Envelope protein; Glycoprotein; Nonstructural Polyprotein; RNA-directed RNA polymerase; Transmembrane. SEQUENCE 3010 AA; 327365 MW; D8653F7317FFA106 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1999) to 1
-1- SIMILARITY: TO HEPATI
EMBL; AF207756; AAF65946
HSSP; P26663; LJXP.
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Genome polyprotein (Contains: envelope glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  progression
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Viruses; ssRNA
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MEROPS; U39.001;
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Characteristics
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NCBI_TaxID=11103;
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                                             (1-633) x Q9J3H7
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tics of hepatitis C viral
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EPATITIS C VIRUS ENVELOPE
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Innogenetics N.V. (BE)
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/db_xref="G1:21712442"
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/db_xref="taxon:11103"
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Other publication AU 3382495
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IMHTPGCVPCVRENNSSGRCWALTPTLAARNASIPTTTRHVDLLVGAAAFCSAMYV
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Patent: US 6245503-A 13 12-JUN-2001;
Location/Qualifiers
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Maertens,G., Bosman,F., De
Purified hepatitis C virus
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                                                    TCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCG
                                                                                                           CTCTTGGCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTG
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              GACATGATCATGCACACCCCCGGGTGCGTTGCCCTGCGTTCGGGAGAACAACTCTTCCCGC
                                                                                              CTCTTGGCTTTACTGTCCTGTCTAACCATTCCAGCTTCCGCTTACGAGGTGCGCAACGTG
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Hepatitis C virus
Viruses; ssRNA positive-strand
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VNYATGNLPGCSFSIFLLALLSCLTIPASAYEVRNVSGMYHVTNDCSNSSIVYEAADM
IMHTPGCVPCVRENNSSRCWVALTPTLAARNASIPTTTIRRHVDLLVGAAAFCSAMYV
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publication AU 3382495
Location/Qualifiers
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VNYATGNLPGCSFSIFLLALLSCLTVPASAYEVRNYCSMYSTVYEAADM
IMHTPGCVPCVRENNSSRCWVALTPTLAARNASVPTTTIRRHVDLLVGAAAFGSANY
GDLCGSVFLVSQLFTISPRRHETVQDCNCSIYPGHTTGHRMAMDMMMNSPTTALVVS
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/db_xref="taxon:32644"
1. .792
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240 c 231 g
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/db_xref="GI:2302381"
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Maertens, G., Bosman, F., De Martynoff,
Purified hepatitis C virus envelope p
therapeutic use
Patent: US 6245503-A 5 12-JUN-2001,
LOCATION/QUalifiers
See 1 . 795
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patent US_6245503.
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Pred. No. 5.1e
0; Mismatches
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5.1e-138;
hes 12;
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proteins

for

diagnostic

linear

PAT 17-OCT-2001

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Indels Length

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Sequence 5 1
AX452754
AX452754.1
                                                                                                                                                                                                                                                                                                                  Hepatitis C
Hepatitis C
Viruses; ssR
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Patent: EP 1
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                                                                                                                                                                                                                                                      Innogenetics
                                                                                                                                                                                                                                                                                                       Hepacivirus
                               Similarity
                                                                       130
                     Conservative
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1.789
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240 c 231 g
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98.1%;
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Patent EP1211315
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                    Score 608.8;
Pred. No. 5.1e
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                                                                                                                                                                                                                           Sequence
A48709
                                                                                        INNOGENETICS NV (BE)
Other publication CA 2172273
Other publication AU 3382495
Location/Qualifiers
                                                                                                                                                 Maertens,G., Bosman,F., De,M.G. and PURIFIED HEPATITIS C VIRUS ENVELOPE
                                                                                                                                                                                      unidentified
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                                                                                                                                Patent: WO 9604385-A 47
                                                                                                                                         THERAPEUTIC
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                                  the conceptual
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: WO9604385.
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Sequence 47
AR157350
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TPSPVVVGTTDRFGVPTYNWGANDSDVLLLNNTRPPRGNWFGCTWMNGTGFTKTCGGP
TPSPVVVGTTDRFGVPTYNWGANDSDVLLLNNTRPPRGNWFGCTWMNGTGFTKTCGGF
TPSPVVVGTTDRFGVPTXNWGANDSDVLLLNTRPPRGNWFYXLLHYYCTVVMFT
IFKVRMYVGGVEHRFEAACNWTRGERCDLEDDRDRSELSPLLSTTEWQILPCSFTTLP
ALSTGLIHLHQNIVDVQVLYGVGSAVVSLVIKWSYVLLLFLLADARICACLWMMLLI
AQAEAALENLYNVLNAAAVAGAHGTLSFLVFFCAAWYIKGRLVPGAAYAFYGVWPLLLL
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/did xref="ci:21712482"
/firanslation="nlckvidtiltcgfadlygyiplygaplggaaralahgyryledg
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gdlcgsyflysglfisprrhetyodcncsiypgittitrhawawdmmnyspttalyys
gdlcgsyflysglfisprrhetyodcncsiypgittyvynllfacydgfrysggaaa
SDTrglvslfspgaamgyllachayysmynmakylvynllfacydgfrykhenssg
CDERLASCRSIDKFACGMFLTYTEPNSSDORFYCWHARPRCGTVPASQYCGFVCF
TPSPVVVGTTDREGYPTYNMGANDSDULILINNTRPPRGNWFGGTVARYGGGP
PCNIGGAGNNTLTCPTDCFRKHPEATYARCGSGFWLTPRCMYTYPYRLWHYPCTVNFT
IFKVRMYYGGYEHRFEBACNWTRGERCDLEDRDRSELSPLLSTTEWDLILCSTTLP
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 TTGGCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCCTTATGAGGTGCGCAACGTGTCC
                                                 GAAGACGGCGTGAACTATGCAACAGGGAATITGCCTGGTTGCTCTTTCTCTATCTTCCTC 183
                                 GAGGACGGCGTGAACTATGCCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC
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publication AU 3382495 960304
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PALSTGLIHLHQNIVDVQYLYGVGSAVVSLVIKWEYVLLLFLLLADARICACLWMMLL
IAQAEAALENLYVLNAAAVAGAHGTLSFLVFFCAAWYIKGRLVPGAAYAFYGVWPLLL
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/db_xref="GI:2302425"
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Maertens,G., Bosman,F., De Martynoff,G. and E
Purified hepatitis C virus envelope proteins
                                                                                                                                                                                                                                                          Unknown
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AX452798
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Hepatitis C virus
Viruses: ssRNA positive-strand
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GVRATRKTSERSOPRGRROP I FKARRPEGRAWADGY PWPLYCHDEGMGMAGWLLSPRG
SRPSWGPTDPRRGSRLAGKVIDTLTGGBADLVGY IPLUGA PLGGAARALHGYRVLED
GVNYATGNLPGCSFS IFLLALLSCLTVPASAYEVRNVSGMYHVNDCSNSS I VEBAD
MIMHTPGCVPCVERNNSSRCWVALTFTLAARNASVFTTI IRRIVDLLVGAARCSAMY
VGDLCGSVFLVSQLFTI SPRRHETVQDCNCS I VPGHITGRRMAMDMMNNSPTTALVV
SQLLRI PQAVVDMVAGAHMGVLAGLAY'SMVGNNAKVLVWMLLFAGVDGHTRVSGGAA
ASDTRGLVSLFSPGSAQKIQLVMTNGSHINRPALNCHNSLOFFFAALFYKHFNSS
GCPERLASCRS IDKFAQGMGPLTYTEPNSSDAPYCMHY PRPCGIVPASQVCGPVYC
FTPSPVVVGTTDAFGVPTNMGANDSUVLILNNTRPPRGNWFGCTWMNGTGFTRTGGF
GPCNIGGAGNNTLTCPTDCFRKHPFATY ARCGGSPWLTPRCMHYPYRLWHYPCTVNF
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/db_xref="taxon:11103"
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Pred. No. 2.9e-137;
0; Mismatches 12;
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Search completed: February 18, 2003, 06:39:08 Job time : 2149 secs

Description

Amino acid sequenc HCV-S1 full-length Infectious hepatit

Non-A, non-B hepat 5'UTR/CORE/ENV/NS1 Hepatitis C virus Cuticle protein 1 NANB hepatitis vir Cuticle protein 1

Infectious hepatit

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Command line parameters:

-MODEL-frame+_n2p.model -DEV-xlp
-MODEL-frame+_n2p.model -DEV-xlp
-Q-/cgn2_1/USPTO_spool/US0989303/runat_12022003_085448_28253/app_query.fasta_1.775
-DB-A_Geneseq_101002 -QFMT-fastan -SUFFIX-n2p.rag -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MRTIX-biosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -QUITMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US0989303_eCGN_1_30_@runat_12022003_085448_28253 -NCPU-6 -ICPU-3
-NO_MAAP -LARGEQUERY -NEG_SCORES-0 -WALT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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08-JUL-1991;
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                                                                                                                                             Non-A non-B hepatitis virus; recombinant; detection.
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AAM47264
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Protein encoded by HCV polypeptide 1.
HK1. Hepatitis C PT-NANBH viral str HCV fusion protein HCV poptide fragme Partial HCV non-st Hepatitis C virus HCV protein cleava Encoded by Hepatit HCV in expression Hepatitis C virus NANB hepatitis C virus Encoded by Protein encoded by HCV core protein prote

Non-A, non-B viral Non-A, non-B viral Non-A, non-B hepat Encoded by Hepatit

Database :

Minimum Maximum

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Scoring table:

BLOSUM62

Xgapop 10.0 Ygapop 10.0 Fgapop 6.0 Delop 6.0

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09-JUL-1990;
30-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 15;
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N-PSDB; AAQ20923.
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        The sequence is that or may be used in a sy. P-733-2. It may may be used in a sy. This method is highly specific and
                                                           Antigen related to non-A and non-B hepatitis virus non-translation region comprising 340 - 341 mols. on non-translation region comprising 1885^{-2} 2551 mols nucleotides including region 1,149 and, etc.
Sequence
                                                Claim 15;
                                                                                                 N-PSDB;
                                                                                                                                   12-JUN-1990;
08-NOV-1990;
                                                                                                                                                                                  JP05091884-A.
                                                                                                                                                                                                             Non-A, non-B;
sensitive; sp
                                                                                                                                                       10-APR-1991;
                                                                                                                                                                                                 Non-A, non-B
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specific;
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90JP-0304405
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                                                                                                                                                                                                                                  gene polypeptide P-733-2
           hepatitis virus HC-OM gene polypeptide in a system for detecting NANB hepatitis. It and sensitive, and can detect NANB not be detected by conventional methods.
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of nucleotides,
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Alignment Pred. No.

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Length:

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Query Match:
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                                                                                    NANB
        07-NOV-1991;
                                                             non-A, non-B hepatitis virus; polymerase chain reaction; var
                     13-MAY-1992
                                                Non-A,
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        91EP-0310297
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97.60%
94.72%
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                                                             vaccine;
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                                                                   NANBHV; PCR; amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the product of the genome of the non-A, non-B hepatitis virus (NANBHY) strain HC-74. This sequence was derived from the DNA sequence which was derived by amplification by polymerase chain reaction. The nucleotide sequences derived from this amplification can be used to detect NANBHY infection which could not be detected by conventional methods. The detection kits allow highly specific and sensitive detection at an early phase of infection. This polypeptide sequence can be used for the manufacture of vaccines and immunological pharmaceuticals and also to produce antibodies specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant cDNA of NANBH virus strain peptides - useful for diagnosis and in pharmaceuticals
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                                                                                                                                  MetIleMetHisThrProGlyCysValProCysValArgGluAspAsnSerSerArgCys
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97.12%
94.11%
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Matches:
Conservative:
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Indels:
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Percent Similarity:
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Query Match:
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                                                                                     US-09-899-303A-7 (1-633) x AAR49537 (1-340)
                                                                                                                                                   Alignment
Pred. No.:
                                                                                                                                                                                           This protein may be expressed in an insect or animal cell culture. The produced ectoprotein can be used in a vaccine and for the diagnosis of HCV infection with high specificity and sensitivity.
                                                                                                                                                                                                                                                 and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus; picorna virus; envelope protein; glycoprotein; ectoprotein; diagnosis; vaccine.
                                                                                                                                                                                                                               Claim 3; Page 31; 45pp; English
                                                                                                                                                                                                                                                         Prodn. of hepatitis C virus ectoprotein - by culturing transformed with DNA encoding the ectoprotein, used in
                                                                                                                                                                                                                                                                                    N-PSDB;
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(NAHE-) NAT INST OF HEALTH JAPAN.
(KOKU-) KOKURITSU YOBO EISEI KENKYUSHO CHO.
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                                     The present invention relates to hepatitis C virus. The present so exemplification of the invention
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                                                                                                                  Disclosure; Page 4-5; 7pp; Korean
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                              non-B hepatitis virus; NANBHV; hepatitis ENV; NS1; NS2; NS3; antigen; detection.
                                              non-B hepatitis virus
                                                                              standard;
                     a
                     virus
                                                         (first entry)
1..191
/label= core
      Location/Qualifiers
1..191
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1081.00
99.04%
95.67%
93.59%
                                                                              Protein;
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                                              gene #6
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus #4 and #6 genes were isolated (AAQ64068-6 Both genes contain the core, ENV, NS1, NS2 and NS3 regions. A core region fragment is given in AAQ64067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SANW ) SANWA KAGAKU KENKYUSHO CO.
(TOFU ) TONEN CORP.
(TOKR-) ZH TOKYOTO RINSHO IGAKU SOGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1992;
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  CGACGCCACGTCGATTTGCTCGTTGGGGCCGCCTGTTTCTGTTCCGCTATGTACGTGGGG
                                                                                 ATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC
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811..1031
/label= NS2-NS3
/note= "NS3 N-terminal"
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                                       Score:
                                                             Alignment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR98362 standard;
                                                                                 Sequence
                                                                                                                                                                  Disclosure; Page 13-15; 15pp;
                                                                                                                                                                                                 Recombinant polypeptide comprising partial NS1 region of hepatitis non-A non-B viral antigen - used in a method for detecting
                                                                                                                                                                                                                                  N-PSDB; AAT30387.
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                                                                                                   sequences given in AAR98361-62 rerpesent the 5'UTR/CORE/ENV/NS1/NS2/protein region derived from hepatitis C virus (HCV) isolates #4 #6 respectively. The proteins partic. contain amino acids 384-of the HCV NS1 antigen. These protein fragments may be used in detection of antibodies against HCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATCTCTGCGGATCTGCTCTCCTCGTCTCCCAGCTGTTCACCATCTCGCCCTCGCCGCAT 543
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384..810
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                                                                                                                            HCV; infectious screening; assay
                          27-JAN-1998;
18-JUL-1997;
                                                                       28-JAN-1999
                                                                                         WO9904008-A2
                                                                                                                                                                                            AAW98022;
                                                                                                                                                                                                             AAW98022 standard; Protein; 3010 AA
      (USSH ) US DEPT
                                                     16-JUL-1998;
                                                                                                           Hepatitis C virus
                                                                                                                                                       Infectious hepatitis C virus genotype 1b strain HC-J4 protein.
                                                                                                                                                                          21-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MetIleMetHisThrProGlyCysValProCysValArgGluGlyAsnSerSerArgCys
                                                                                                                           assay;
                                                                                                                                                                         (first entry)
                          98US-0014416.
97US-0053062.
                                                     98WO-US14688
                                                                                                                            clone; infection; diagnosis; therapy; vaccine;
y; antiviral; virucide.
       HEALTH & HUMAN SERVICES
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This protein is encoded by the infectious hepatitis C virus (HCV) composition of the protein is encoded by the infectious hepatitis C virus (HCV) composition of the produce of the produce chimeric genomes (see AAX24833). HC-J4 was obtained containing HC-J4/91. The infectious nucleic acid sequence can be used to produce chimeric genomes (see AAX24833) consisting of the open reading frames of infectious nucleic acid sequences of other genotypes (including genotypes 1-6) and subtypes (such as 1b, 2a, 2b, 2c, 3a, 4a-f, 5a and 6a) of HCV. The invention also relates to the introduction of mutations or deletions into infectious nucleic acid sequences in order to produce an attenuated HCV virus suitable for vaccine development. Infectious nucleic acid sequences can also be used to produce attenuated virus via passage in vitro or in vivo of the viruses produced by transfection of a host cell with the infectious nucleic acid sequence. Vaccines comprising one or more polypeptides made from the infectious nucleic acid sequence are used to immunise mammals, especially humans, against hepatitis C. The nucleic acid sequences can also be used to induce protective immunity against the virus. The nucleic acid sequences or their encoded proteases (e.g. NS3 protease) can additionally be used to develop screening assays to identify antiviral agents for HCV.
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 14G-H; 126pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated hepatitis C virus nucleic acids - used to develop products for the diagnosis, prevention and treatment of HCV infections and for developing screening assays
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US-09-899-303A-7 (1-633) x AAW98022 (1-3010) 5.46e-104 1081.00 98.56% 95.67% 93.59%

Query Match:

Percent Similarity: Best Local Similarity:

Score: Pred. No.: Alignment Scores:

Length: Matches:

Mismatches: Indels: Conservative:

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                             Alignment
                                                                                                                      genome, specifically bovine viral diarrhoea virus (BVDV) genome in which the (non-)structural region has been replaced by the (non-)structural region of a hepatitis C virus (HCV) genome. The nucleic acids comprising the chimeric virus and the chimeric virus are useful for identifying cell lines capable of supporting the replication of these chimeric viruses, in screening for neutralizing antibodies to HCV of different genotypes, in the production of HCV-BVDV virions, for the development of inactivated or attenuated vaccines to prevent HCV-BVDV in a mammal, in studying the melecular properties of HCV indirectly in vitro, and in identifying inhibitors of viral enzyme activity which would be useful as antiviral agents. Formulations or compositions comprising the
                                                                                                              chimeric
                                                       Sequence
                                                                                                                                                                                                                                                                                The specification describes a nucleic acid comprising a chimeric virus
                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4G-H; 97pp; English
                                                                                                                                                                                                                                                                                                                                                  New nucleic acid comprising a chimeric bovine viral diarrhoea virus genome in which the (non-)structural region has been replaced by hepatitis ( Virus (HCV) genome useful for treating or preventing HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-2000; 2000WO-US15527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric virus; bovine viral diarrhoea virus; BVDV; hepatitis C virus; HCV; vaccine; viral inhibitor; antiviral.
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DB; AAC86939.
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                                                                                                                                                                                                                                                                                                                                           and symptoms
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                                                                                virions may be used to treat or prevent the signs The present sequence is encoded by a HCV clone, whi ruct chimeric nucleic acids of the invention.
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                                                                     Nucleic acid construct; expression cassette; non-coding region; NCR; untranslated region; UTR; anti-viral drug; drug resistance; HCV-S1; Hepatitis C virus.
                      31-JAN-2002
                                                                                                                      01-JUL-2002
                                                      Hepatitis C virus
                                                                                                     HCV-S1 full-length
                                                                                                                                      AAE20477;
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                                                                                                                     (first entry)
                                                                                                      polyprotein.
                                                                                                                                                      Protein;
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24-JUL-2000;

2000US-220248P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC expression cassette including a first polynucleotide region including cassette including a first polynucleotide region including cc a 5' non-coding region (NCR) sequence of an RNA virus and at least an CC N-terminal portion of a coding sequence of RNA virus, a second coding coding coding sequence of RNA virus, a second coding coding coding coding coding sequence of the RNA virus and at least a C-terminal portion of a coding sequence cc of the virus and at hird polynucleotide region encoding a reporter cc molecule, flanked by first and second polynucleotide regions; and a cc promoter sequence being operatively linked to expression cassette in a cc manner so as to enable a transcription of a minus strand RNA molecule from the expression cassette. Nucleic acid construct of the invention cc is useful for detecting the presence of an RNA virus in a cell. It is calso useful for screening anti-viral drugs and determining drug cresistance of an RNA virus. The present sequence is Hepatitis C virus cx (HCV) isolate HCV-S1 full-length polyprotein.
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y Match:
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                                               TrpValAlaLeuThrProThrLeuAlaAlaArgAsnLeuSerValProThrThrThrIle
                      TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCCAGCGTCCCCACTACGACAATA
                                                                                                                                                          TTGGCTTTACTGTCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTGTCC
                                                                                                                                                                                                                                                                   2002-280605/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               id construct useful for detecting the presence of RNA an expression cassette and a promoter operably linked ssette for minus strand RNA transcription of the
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comprises the nonstructural region of infectious genotype la strain comprises the nonstructural region of infectious genotype la strain comprises the nonstructural region of infectious genotype (CC ib strain HC-74 (see AAW98021). The construction of such chimeric comcleic acid sequences is expected to be of importance in studying complete the growth and virulence properties of HCV and in the production comprises of HCV. The invention also relates to the introduction comprises of HCV. The invention also relates to the introduction comprises of HCV. The invention also relates to the introduction composed to the introduction composed to include the produce an attenuated HCV virus suitable for vaccine comproduce an attenuated HCV virus suitable for vaccine comproduce attenuated virus via passage in vitro or in vivo of the composed to immunise mammals, especially humans, against hepatitis C. The nucleic acid sequences can also be used to immunise mammals, especially humans, against hepatitis C. The nucleic acid sequences or their composed proteases (e.g. NS3 protease) can additionally be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated hepatitis C virus nucleic acids \cdot used to develop products for the diagnosis, prevention and treatment of HCV infections and for developing screening assays
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                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR25854-74 are hepatitis C virus protiens. The genes encoding these proteins can each be used to prepare recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vectors by ligating the gene of interest in to a vector recombinant vector vector vectors.
                                                                                                                                                                                                                                                                                                                                                                                                    to be expressed in E. coli. These polypeptides diagnostic reagents for type C hepatitis and the efficiently by recombinant methods.
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RESULT 15
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protein
                                                                                                                                                         Disclosure;
                                                                                                                                                                                                 Hepatitis C virus antigen expressed useful for diagnosis of hepatitis C
                                                                                                                                                                                                                                                                        N-PSDB;
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The sequences given in AAR25876-95 are encoded C virus genes of the invention which have been coli vector. These polypeptides are useful as for type C hepatitis and they may be produced e

d by the claimed hepatitis
n inserted into an E.
s diagnostic reagents
efficiently by

recombinant DNA techniques

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Minimum
Maximum
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-MODEL-frame+_nlp.model -DEV-xlp
-Q-/cgn2_1/USPTQ_Spool_VG0989303/runat_12022003_085450_28314/app_query.fasta_1.775
-Q-/cgn2_1/USPTQ_Spool_VG0989303/runat_12022003_085450_28314/app_query.fasta_1.775
-DB-Iasued_Patents_AA -QPMT-fastan -SUFFIX-nlp.rai -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTEMT-pto -NORM-scrt -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09899303_@CGN_1_1_12_@runat_12022003_085450_28314 -NCPU-6 -TCPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Maximum Match 100%
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US-08-927-597-14
US-08-927-597-48
US-08-927-597-48
US-08-927-597-59
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US-08-612-973-8
                                                         STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT IMFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 12,205
REFERENCE/DOCKET NUMBER: 1487-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6150134
GENERAL INFORMATION:
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  INFORMATION FOR
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS
TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                           TELEPHONE: (703)
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CITY: ARLINGTON
STATE: VIRGINIA
                         TELEFAX:
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1100 NORTH GLEBE ROAL
                       (703)
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US-08-394-616-12
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Result

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Sequence 8, Application US/08927597;
Patent No. 6245503;
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: BOSMAN, FONS
APPLICANT: BUSE, MARIE-ANGE
APPLICANT: BUYSE, MARIE-ANGE
TIPLE OF INVENTION: PURIFIED HE
TITLE OF INVENTION: PROTEINS FOR NUMBER OF SEQUENCES: 111
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US-08-612-973-8
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LENGTH: 209 amino acid
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REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 209 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,597
FILING DATE:
CLASSIFICATION:
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ADDRESSEE: NIXON
STREET: 1100 NOR!
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
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TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 816-410
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4400
TELEPAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
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TOPOLOGY:
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CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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                ATTORNEY/AGENT INFORMATION: NAME: BYRNE, THOMAS E.
                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS
                                                                                            PRIOR APPLICATION DATA:
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                                                      APPLICATION NUMBER: US 08/612,973 FILING DATE: 11-MAR-1996
                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 22201-4714
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Patent NO. 6150134
GENERAL INFORMATION:
APPLICANT: MAERTENS, G
APPLICANT: BOSMAN, FON
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
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  MAERTENS, GEERT
BOSMAN, FONS
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Matches:
Conservative:
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Indels:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT IMFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487-10
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
TELEPAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (703) 816-410 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 111
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STREET: 1100 NORT
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
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TYPE: amino acid
TOPOLOGY: linear
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                                           AspMetIleMetHisThrProGlyCysValProCysValArgGluAsnAsnSerSerArg
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1100 NORTH GLEBE ROAL
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FOR DIAGNOSTIC AND THERAPEUTIC USE
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Query Match:
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US-08-927-597-14
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                                                        Percent Similarity:
Best Local Similarity:
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US-09-899-303A-7 (1-633) x US-08-927-597-14 (1-210)
                                                                                         Score:
                                                                                                           Pred. No.:
                                                                                                                         Alignment Scores:
                                                                                                                                                       ; MOLECULE TYPE: US-08-927-597-14
                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/612
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487
TELECOMMUNICATION INFORMATION:
TELEPIAN: (703) 816-4100
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
I ENGREE 1 20 20 426
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                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,59;
FILING DATE:
CLASSIFICATION:
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MEDIUM TYPE: Floppy disk
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APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PROTEINS FOR DIAGNOSTIC AND THERAPEUTIC USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NOR CITY: ARLINGTON STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                          TYPE: amino acids
TOPOLOGY: line
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6245503
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1100 NORTH GLEBE ROAD
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Matches:
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Indels:
                                                                            Conservative:
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Sequence, Sequence, Sequence, Patent No. 615012.

Patent No. 615012.

GENERAL INFORMATION:

APPLICANT: MAERTENS, GEERT

APPLICANT: BOSMAN, FONS

APPLICANT: BOSMAN, FONS

APPLICANT: BUYSE, MARIE-ANGE

TOTAL OF INVENTION: PROTEINS FO
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US-08-612-973-48
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       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, vc
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
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ATTORNEY/AGENT INFORMATION
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                                                                                                                     COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                            CITY: ARLINGTON
STATE: VIRGINIA
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1100 NORTH GLEBE ROAD
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FOR DIAGNOSTIC AND THERAPEUTIC USE
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RESULT 8
US-08-927-597-48
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Best Local Similarity:
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TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
INFORMATION: FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 692 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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Matches:
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REFERENCE/DOCKET NUMBER: 32,205

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 815-4000
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 ----
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Best Local Similarity:
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APPLICANT: BOSMAN, FONS
APPLICANT: DE MARTYNOFF, GUY
APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED H
TITLE OF INVENTION: PROTEINS F
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08 FILING DATE: 11-MAR-1996 ATTORNEY/AGENT INFORMATION: NAME: BYRNE THOMAS E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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              304
                                     124 GAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTCTATCTTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 692 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                          184
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                                                                                                                                                     GluAspGlyValAsnTyrAlaThrGlyAsnLeuProGlyCysSerPheSerIlePheLeu
E: NIXON & VANDERHYE P.C.
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FOR DIAGNOSTIC AND THERAPEUTIC USE
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REFERENCE/DOCKET NUMBER: 32,205

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 815-400
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: SAAA.—.
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Query Match:
DB:
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                                                              Alignment Scores:
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GENERAL INFORMATION:
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APPLICANT: BUYSE, MARIE-ANGE
TITLE OF INVENTION: PURIFIED |
TITLE OF INVENTION: PROTEINS
TITLE OF SEQUENCES: 111
                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,973
FILING DATE: 11-MAR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                        LENGTH: 809 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 22201-4714
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DE MARTYNOFF, GUY
BUYSE, MARIE-ANGE
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                                                                                                                                                                                                                                    Patent No.
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RESULT 10
US-08-927-597-50
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                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                             APPLICANT: BUYSE, MARIE ANGE
TITLE OF INVENTION: PURIFIED
TITLE OF INVENTION: PROTEINS
TITLE OF SEQUENCES: 111
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                            ADDRESSEE: NIXON & VANDERHYE |
STREET: 1100 NORTH GLEBE ROAD
CLTY: ARLINGTON
STATE: VIRGINIA
COUNTRY. TECHNICAL
                                                                                            COUNTRY:
ZIP: 222
                                                           COMPUTER:
APPLICATION NUMBER: FILING DATE:
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                                                                                          22201-4714
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BUYSE, MARIE-ANGE
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PRIOR APPLICATION DATA: APPLICATION NUMBER:

CLASSIFICATION:

FILING DATE:

11-MAR-1996

US 08/612,973

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DB:
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECCULE TYPE: protein
US-08-927-597-50
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Best Local Similarity:
Query Match:
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NAME: BYRNE, THOMAS E.
REGISTRATION NUMBER: 32,205
REFERENCE/DOCKET NUMBER: 1487
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPHONE: (703) 816-4100
TELEPHONE: (703) 816-4100
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 809 annino acids
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                                                                   AspLeuCysGlySerValPheLeuValSerGlnLeuPheThrIleSerProArgArgHis
                                                                                     GATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT 543
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Conservative:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/446,303
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: JP 152487/1992
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5789544man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4169-003-0
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT: MIYAMU
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: SEKI, MAKOTO
TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROTEIN OF
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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     124
                                                                                               STREET: 1755 S.
CITY: Arlington
STATE: Virginia
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RESULT 12
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Patent No.
 APPLICATION NUMBER: US/08/446,303
FILING DATE:
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-UUN-1993
APPLICATION NUMBER: JP 152487/1992
FILING DATE: 11-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5830691man F.
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLICANT: MIXAUDRA, TATSUO
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: HANDA, YOSHIKAZU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: SEKI, MAKOTO
TITLE OF INVENTION: HEPHOD FOR PRODUCING ECTOPROTEIN
TITLE OF INVENTION: HEPHOTIS C VIRUS
TITLE OF INVENTION: HEPHOTIS C VIRUS
TORRESPONDENCE ADDRESS:
                                                                                                MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/636,883
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION ADATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
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1755 S. Jefferson Davis Highway, Suite
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEFX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-636-883-2
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                                   RESULT 13
US-09-127-829-2
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Query Match:
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Best Local Similarity:
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Sequence 2, Application Patent No. 6063904 GENERAL INFORMATION:
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                                                                                                                      GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCCGGCCACATAACAGGTCACCGTATG
                                                                                                                                                                        TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACATA
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                                                                                    GCTTGGGATATGATGATGAACTGG 627
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                                                                          AlaTrpAspMetMetMetAsnTrp
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DATE:
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,829
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MENTUM TYPE: Floppy disk
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TITLE OF INVENTION: METHOD FOR PRODUCING
TITLE OF INVENTION: HEPATITIS C VIRUS
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NAME: Oblon, No. 6063904man
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APPLICANT: Emerson, Susanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: CLONED GENOMES OF INFECT
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 20264276
CURRENT APPLICATION NUMBER: US/09/014,416
CURRENT FILING DATE: 1998-01-27
EARLIER APPLICATION NUMBER: US 60/053,062
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 3010
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APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES.
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 20264276
CURRENT APPLICATION NUMBER: US/09/014,416
CURRENT FILING DATE: 1998-01-27
EARLIER APPLICATION NUMBER: US 60/053,062
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Bukh, Jens
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ALIGNMENTS

RESULT 1 AAT12706 AAT12706 standard; DNA; 633 BP. W09604385-A2. AAT12706; (INNO-) INNOGENETICS NV. 31-JUL-1995; 15-FEB-1996. HCV; E1; HCV El construct HCCIllA. Bosman F, 29-JUL-1994; Hepatitis C virus. serotype; 23-SEP-1996 (first entry) E2; disulphide bond cleavage; envelope protein; vaccine; human; reversed phase hybridisation assay; genotype; antigen; sera; Buyse M, 94EP-0870132 95WO-EP03031 De Martynoff G, Maertens

Purifying recombinant hepatitis C virus (HCV) El and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to

WPI; 1996-129401/13.

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ATGGCTTGGGATATGATGATGAACTGGTAATAG
               ATGGCTTGGGATATGATGATGAACTGGTAATAG
                                                              CATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGT
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                                                                                                                      Query Match
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m C} and E2 protein coding sequence constructs. These sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purifying recombinant hepatitis C virus (HCV) E1 and E2 envelope proteins - in presence of di:sulphide bond cleavage agent, to produce proteins suitable for direct use in vaccines or diagnost:
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                     Purifying recombinant hepatitis C virus (HCV) El and proteins - in presence of di:sulphide bond cleavage produce proteins suitable for direct use in vaccines assays of HCV
      Claim
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                                                                                               (INNO-) INNOGENETICS
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; reversed phase hybridisation
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      146pp; English
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 795
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                                                                                                      CTCGTCGGCCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTG
                                                            GAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTCTATCTTCCTC
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                                             GAGGACGGCGTGAACTATGCCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTC
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                                                                   Claim 23;
                                                                                        Purifying recombinant hepatitis C virus (HCV) El and proteins - in presence of disulphide bond cleavage produce proteins suitable for direct use in vaccines assays of HCV
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               26-0CT-1998
                                                                 AAV42305 standard;
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                                                                                                                                                GCTTGGGATATGATGATGAACTGGT
                                                                                                                                                                                                                                                        GATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCCTCGCCGGCAT
                                                                                                                                                                                                                                                                                                            CGACGCCACGTCGATTTGCTCGTTGGGGCCGCCTTTCTGTTTCCGCTATGTACGTGGGG
                                                                                                                                                                                                                                                                                                                                                  TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACAATA 423
                                                                                                                                                                                                                                                                                                                                                                                                                     ATGATCATGCACACCCCCGGGTGCGCTGCCCTGCGTTCGGGAGAACCAACTCTTCCCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTG 123
                                                                                                                                                                                                                GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATG
                                                                                                                                                                                                                                          GACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
                                                                                                                                                                                                                                                                                              CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                       ATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
            (first entry)
                                                                 CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.7%;
98.1%;
                                                                 673
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                                                                 ВP
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                                                                                                                                                           628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.2e-158;
nes 12;
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vaccine; ds.
                                                                                                                                    infection; hepatitis
                                                                                                                                              HCV core protein cDNA insert of
                                                                                                                                    hepatitis D virus; L-HDAg; virus-like particle; is B virus surface antigen; 'HBsAg; immunogen;
                                                                                                                                              plasmid
                                                                                                                                              pA10.
```

Hepatitis C virus

W09828004-A1

02-JUL-1998

24-DEC-1997; 97WO-AU00884

24-DEC-1996;

96AU-0004341

(QUEE-) QUEENSLAND DEPT HEALTH SAKZEWSKI VIRUS

Gowans EJ, MacNaughton TB;

1998-377411/32 AAW62825

Virus-like particle for, e.g. treating microbial infection comprises polypeptide from microorganism and sequence from Hepatitis D virus large protein, partially enveloped by Hepatitis B surface antigen

Example; Fig 4. 72pp; English

This nucleotide comprises the hepatitis C virus (HCV) cDNA insert in plasmid pA10. This cDNA was obtained by PCR amplification of HCV cDNA using primers (see AAV38849-50) designed to amplify the HCV cDNA using primers (see AAV38849-50) designed to amplify the CTPA core gene. The PCR product was cloned into pBluescript KS to create pA10. It encodes a 224-amino acid polypeptide (see AAW62825). The HCV core protein can be used as an immunogen in novel fusion proteins (see AAW62657-59) that comprise HCV core protein and at least 19 amino acids (see AAW62827) of the C-terminal sequence of the large protein from hepatitis D virus (L-HDAg). In novel virus-like particles of the invention, a fusion protein immunogen is at least partially enveloped by hepatitis B surface antigen. The virus-like particle is used to ameliorate or protect against infections caused by hepatitis B virus and/or another microorganism, especially HCV. Sequence BP; 115

A; 208 C; 188 G; 162 T; 0 other;

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Š
                           Query Match
Best Local Similarity
Matches 587; Conserv
GGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTC 66
                           Conservative
                                      89.2%;
                          0;
                                      Score 564.8; DB 19;
Pred. No. 5.1e-147;
                           Mismatches
                           Indels
                          0,
                          0
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В	Qγ	밁
61 GTCGGCGCCCTCTAGGGGGCCCCGCCAGGGCCCTGGCGCATGGCGTTCCGGGTTCTGGAG 120	67 GTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCCTGGCGCATGGCGTCCGGGTTCTGGAA 126	1 GGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTC 60

ДЬ		Qγ
121		127
121 GACGGCGTGAACTATGCAACAGGGAATTTTGCCCGGTTTGCTCTTTCTCTATCTTCCTCTTG 180		127 GACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCTTG 186
G 180	_	G 186

TGG -	301 ATCATGCACGTCCCCGGGTGCCCTGCGTTCGGGTGGACAACTCCTCCCGTTGCTGG 360	301	망
GCTGCTGG	307 ATCATGCACACCCCCGGGTGCCGTGCCTTCGGGAGAACAACTCTTCCCGCTGCTGG 366	307	Qy
CGGACATG	241 GTGTACCATGTCACGAACGGCTCCAACGCAAGCATTGTGTATGAGGCAGCGGACATG 300	241	B
CGGACATG	247 ATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGACATG 306	247	Qy
TGTCCGGG	181 GGTTTGCTGTTTGATTGACCATCCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCCGGG 240	181	망
TGTCCGGG 246	187 GCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTGTCCGGG	187	Qγ

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RESULT 7
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ID ABA(
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                Query Match
Best Local Similarity
Matches 588; Conserv
                                                                                                          The present invention relates to cuticle protein 1 and 2 secreting hepatitis C virus. The present sequence is a coding sequence provided in the exemplification of the invention.
                                                                                                                                                                                                                                                       WPI; 1998-492654/42.
P-PSDB; AAM47264.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                          Cuticle protein 1 and 2 secreting hepatitis C NoAbstract - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-1997.
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                                                                              Sequence
                                                                                                                                                                          Disclosure; Page 2–4; 7pp; Korean.
                                                                                                                                                                                                                                                                                                       Choo SH,
                                                                                                                                                                                                                                                                                                                                                                      19-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cuticle protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA03491;
                                                                                                                                                                                                                                                                                                                                      (GLDS ) LG CHEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGGATATGATGATGAACTGGTAA 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTGCGGATCTGTTTTCCTCGTCGCCCAGCTGTTCACCTTCTCGCCCCGCCGGCATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein 1 and 2 secreting hepatitis C virus related DNA
                                                                                2187
                                                                                                                                                                                                                                                                                                       Lee IH,
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                             BP;
                                                                                                                                                                                                                                                                                                                                                                      96KR-0007404.
                                                                                                                                                                                                                                                                                                                                                                                                     96KR-0007404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; cuticle protein
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/note= "
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/product= "AAM47264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1..2187
                                                                             406 A; 669 C; 631 G;
                                                                                                                                                                                                                                                                                                       Ryoo
                             89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "no stop codon"
                Score 564.6; DB 19
Pred. No. 8.7e-147;
0; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hepatitis C virus;
                                                                              481 T; 0 other;
                                             DB 19;
                                                                                                                                                                                                                        virus (Japanese)
                   Indels
                                            Length
                                               2187;
                0;
                Gaps
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ARESULT 8
AAQ43889
ID AAQ4
XX AAQ4
XX 21-0
DT 21-0
XX NOn-
KW Sens
XX NOn-
XX NOn-
XX NOn-
XX ST CDS
FT CDS
FT CDS
FT 5'UT
FT 5'UT
XX AAQ4
XX JF05
XX AAQ4
XX AAQ4
XX NOn-
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                                                                                                                                         5'UTR
                                                                                                                                                                                                                                                      Non-A, non-B; virus; sensitive; specific;
                                                                                                                                                                                                                                                                                                    NANB hepatitis virus polynucleotide N-2540-2
                                                                                                                                                                                                                                                                                                                                                                                                 AAQ43889 standard; cDNA
                10-APR-1991;
                                                                             JP05091884-A.
                                                                                                                                                                                                                        Non-A,
                                                                                                                                                                                                                                                                                                                                      21-OCT-1993
                                               16-APR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTTCCGCTATGTACGTGGGG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTTCCGGGTTCTG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACAATA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCGGGAGAACAACTCTTCCCGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTTGGGATATGATGATGAACTGGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTTGGGATATGATGATGAACTGGTAA
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                                                                                                                                                                                                                          non-B
                                                                                                                                                                                                                        hepatitis virus
                                                                                                                                                                                                                                                                                                                                   (first entry)
              91JP-0196175
                                                                                                                                           /*tag=
1..341
                                                                                                                                                                          Location/Qualifiers 342..2540
                                                                                                              /note-
                                                                                                                            /*tag=
                                                                                                                                                                                                                                                    polymerase chain reaction; HCV; NANBH; ss.
                                                                                                          "from
                                                                                                                                                                                                                                                                                                                                                                                                 to mRNA;
                                                                                                            ű
                                                                                                            terminal of NANBH virus
                                                                                                                                                                                                                                                                                                                                                                                                 2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630
                                                                                                                                                                                                                                                                        detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen related to non-A and non-B hepatitis virus non-translation region comprising 340 - 341 mols. of non-translation region comprising 1885 - 2551 mols. nucleotides including region 1,149 and, etc.
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                                                        GATCTCTGCGGATCTGTCTCCCCGTCTCCCAGCTGTTCACCATCTCGCCTCGCCGGCAT
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                            GAGACAGTGCAGGACTGCAACTGCTCAATCTATCCCGGCCATTTATCAGGTCACCGCATG
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588; Conserv
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90JP-0304405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide primer virus - used for high s hepatitis virus
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non-A, non-B
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TGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCGTCCCCACTACGACATA
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The invention relates to Hepatitis C virus (HCV) variants which include CC polynucleotides comprising non-naturally occurring HCV sequence and HCV CC variants that have a transfection efficiency and ability to survive Subpassage greater than HCV that have wild-type polyprotein coding CC regions. The polynucleotides of the invention are useful for identifying CC acell line that is permissive for infection with HCV and detecting CC replication of HCV in cells of the cell line. They are also useful for CC testing a compound for anti-viral properties and for inhibiting HCV CC infection. They are also useful for the generation of defined HCV virus CC stocks to develop in vitro and in vivo assays for virus neutralisation, CC attachment, penetration and entry, structure/function studies on HCV CC proteins and RNA elements and identification of new antiviral targets, CC a systematic survey of cell culture systems and conditions to identify CC chose that support wild-type and variant HCV RNA replication and CC particle release, production of adaptive HCV variants capable of more celficiency replication in cell culture, production of alternative animal
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                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus variants having greater transfection efficiency and ability to survive subpassage, useful as a vaccine for immunizing primate to the virus, comprise non-naturally occurring viral sequence.
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gene therapy; vaccine; immunoprotection; hepatotropic; virucide; liver;
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                                                                                                                                                                                                                                                                                                                  Page 97-100;
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RESULT 1
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AC AAD
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AAD25331 standard; cDNA; 11062

ВP

AAD25331; 12-MAR-2002

(first entry)

Hepatitis C virus (HCV) full-length cDNA mutant

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Best Local Similarity
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GCTTGGGATATGATGAACTGGTCA 1322
                GCTTGGGATATGATGATGAACTGGTAA 630
                                                         GAGACAGTACAGGACTGCAATTGCTCAATATATCCCCGGCCACGTGACAGGTCACCGTATG
                                                                        GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACAGGTCACCGTATG
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93.8%;
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tches 39;
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                                                                                                                                                                     CC polyniclectides comprising non-naturally occurring HCV sequence and HCV covariants that have a transfection efficiency and ability to survive convariants that have a transfection efficiency and ability to survive convariants that have a transfection efficiency and ability to survive convariants that have a transfection are useful for identifying converges. The polynucleotides of the invention are useful for identifying care acell line that is permissive for infection with HCV and detecting converges are also useful for the generation are also useful for testing a compound for anti-viral properties and for inhibiting HCV confection. They are also useful for the generation of defined HCV virus for the generation of defined HCV virus stocks to develop in vitro and in vivo assays for virus neutralisation, converges and the entities of the survey of cell culture systems and conditions to identify those that surport wild-type and variant HCV RNA replication and converges that support wild-type and variant HCV RNA replication and converges that support wild-type and variant HCV variants capable of more efficiency replication in cell culture, production of HCV variants with altered tissue or species tropism, establishment of alternative animal conditions of immunogenic HCV particles for vegolication assays, and conditions of immunogenic HCV particles for vegolication assays. Conditions of immunogenic HCV particles for vegolication assays, and for utilisation of the HCV plycoproteins for targetted delivery of thereapy and vaccine applications of attenuated or defective HCV particles for vaccine applications of immunogenic HCV particles for vaccine applications of immunogenic HCV in a primate. The present sequence is useful for inducing that results in Ser to lie at position 1179 of HCV replibartMan protein, where the 5'NTR is fused to the neomycin phosphotransferase gene and conditions of the EMCV IRBS is inserted upstream of the HCV open reading frame.
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Best Local S
Matches 588
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                                                                                                                                                    Sequence 11062
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            CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is C virus variants having greater transfection to survive subpassage, useful as a vaccine for to the virus, comprise non-naturally occurring
                                                                                                          Similarity
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                                                                                              Conservative
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Pred. No. 1.
                                                                                                          Pred.
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hes 39;
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                                     Cell culture system for hepatitis C virus, useful e.g. in screening for therapeutic agents, comprises human hepatoma cells containing a viral RNA construct that includes a selectable gene -
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           Page 14-22; 58pp;
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            German
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Cell culture; therapy; infection; vaccine; diagnosis;
(UYMA-) UNIV MAINZ GUTENBERG JOHANNES
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RESULT 13
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                                          1880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 564.6; DB 21
Pred. No. 1.5e-146;
0; Mismatches 39;
                                                                                                                                  2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches 587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the genome of the non-A, non-B hepatitis virus (NANBHV) strain HC-J4. This sequence was derived by amplification by polymerase chain reaction. The nucleotide sequences derived from this amplification can be used to detect NANBHV infection which contropy the detected by conventional methods. The detection kits allow highly specific and sensitive detection at an early phase of infection. The polypeptide product of this coding sequence can be for the manufacture of vaccines and immunological pharmaceuticals and also to produce antibodies specific to NANBHV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant cDNA of NANBH virus strain peptides - useful for diagnosis and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-A, non-B hepatitis virus; NANBHV; PCR;
polymerase chain reaction; vaccine; antiboo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NANB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1880 BP; 333 A; 593 C; 556 G; 398 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 11; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceuticals
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                                      936
                                                                                                             876
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                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                     4 TTGGGTAAGGTCATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGGTACATTCCG
                                                                                                                                                                                   GAAGACGGCGTGAACTATGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTC 183
                                                                                                                                                                                                                                                            CICGTCGGCGCCCCTAGGGGGCGCTGCCAGGGCCTTGGCACACGGTGTCCGGGTTCTG
                                                                                                                                                                                                                                                                                             CTCGTCGGCGCCCCCTAGGGGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1992-160959/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hepatitis virus strain HC-J4 genome.
                                                                                                           TIGGCTTTGCTGTCCTGTTTGACCATCCCAGCTTCCGCTTATGAAGTGCGCAACGTGTCC
                                                     GGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGAC
                                                                                                                                               TTGGCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTGTCC
                                                                                                                                                                                                                                                                                                                                 TTGGGTAAGGTCATCGATACCCCTACATGCGGCTTCGCCGATCTCATGGGGTATATTCCG 755
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90JP-0304405
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/label= HC-J4
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                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 563; DB 13,
Pred. No. 2.3e-146;
"""matches 40;
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                                                                                                                                                                                           20-DEC-1990;
09-JUL-1990;
30-NOV-1990;
                 The sequence is that of a DNA fragment encoding a non-A non-B (NANB) hepatitis-specific antigen polypeptide, it can be used to produce the polypeptide recombinantly. It is derived from the DNA clone C10-E12. It can be used to give PCR primers which are capable of detecting NANE hepatitis with high accuracy. See also AAQ20617-Q20629 and AAQ20922-Q20926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1296
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                                                                                 Claim 15;
                                                                                                 Non-A, non-B hepatitis-specific antigen polypeptide - for of hepatitis virus gene or antibody directed against virus
                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                08-JUL-1991;
                                                                                                                                                                                                                                                                    EP468657-A.
                                                                                                                                                                                                                                                                                                                                                             C10-E12 DNA
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DB; AAR20720.
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                                                                                                                                                                                                                                                                                                                         non-B
                                                                                                                                                       Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                Fig 15; 78pp;
                                                                                                                                                                                                                                                                                                                                                           fragment encoding NANBH-specific antigen polypeptide
                                                                                                                                                                                                                                                                                                                        hepatitis virus.
                                                                                                                                                                                                                                                                                                                                          hepatitis virus;
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                           CORP.
                                                                                                                                                                                          90JP-0413844.
90JP-0180889.
90JP-0339589.
                                                                                                                                                                                                                               91EP-0306158
                                                                                                                                                                                                                                                                                    Location/Qualifiers
3..932
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                                        Toyoshima
                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                  932
                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                          recombinant; detection;
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                                                                                                                                                         Kohara
                                                                                                            for detection
                                    NANB
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Best Local Similarity
Matches 586; Conserv
                                            26-APR-1991;
                                                                                   23-APR-1992;
                                                                                                                                                                  EP510952-A.
                                                                                                                                                                                                                                              Non-A non-B
PCR; primer;
                                                                                                                                                                                                                                                                                                            Hepatitis C
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                                                                                                                                                                                                                                                                                                                                                                                             AAQ29628;
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                                                                                                                                                                                                        Hepatitis
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                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                hepatitis; NANBH; polymerase chain
                                                                                                                                                                                                      virus.
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93.5%;
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reaction; ss.
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                                                                                                                                                                                                                                                                    diagnosis; screening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of non-A, non-B hepatitis virus - using new oligo-nucleotide primers with nucleotide sequences corresp. part. of the viral RNA
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                                                                                                                  GAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCCGGCCACATAACAGGTCACCGTATG 603
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                                                                                                                                                                                                                                                                       CGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCTCCGCTATGTACGTGGGG 1175
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                                                                                      GAGACAGTGCAGGACTCCAACTGCTCAATCTATCCCGGCCATTTATCAGGTCACCGCATG
                                                                                                                                                                                   GATCTCTGCGGATCTGTTTTCCTCGTCTCCCAGCTGTTCACCTTCTCGCCTCGCCGGCAT
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GCTTGGGATATGATGATGAACTGGTCA 1322
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Search completed: February 18, 2003, 06:03:10 Job time: 237 secs

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ALIGNMENTS

TITLE JOURNAL COMMENT RESULT 1 AV755731/c LOCUS REFERENCE AUTHORS SOURCE ORGANISM DEFINITION ACCESSION VERSION FEATURES KEYWORDS source Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 488)

Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z. Homo sapiens cDNA BM clones

Unpublished (2000) human. AV755731 M Homo sapiens cDNA clone BMFAKB03 5', mRNA sequence.
AV755731 GI:10913579 Email: hanzg@chgc.sh.cn This clone is available at CHGC Homo sapiens Location/Qualifiers /organism="Homo sapiens" . 488 j Shanghai. EST 19-OCT-2000

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AV758366
AV758366
                                                                                                                                                                                                                                                                                Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G
Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
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                                                                                                                                                                                                                                   hanzg@chgc.sh.cn
lone is available at CHGC
Location/Qualifiers
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                                                                                                         /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25 8"
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/clone="BMFAKB03"
                                                                                             /note="Vector:
                                                                                                                                                                        /clone="BMFAKA03"
                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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134 c 137 g 97 t 4 others
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Pred. No. 1.1e-05;
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   AGTGCGCCTTGCGTGCTCCGTGCTCTCTCGGCCGCTGACATCCTGGCCGTCTGCCCTC 1066
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Plate: LLAM11003 row: a column:
High quality sequence start: 6
High quality sequence stop: 416.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/Clone_lib="NCI_CGAP_CO24"
/Clone_lib="NCI_CGAP_CO24"
/Clone_lib="NCI_CGAP_CO24"
/Lab_host="DH10B (Tl phage-resistant)"
/Inote="Organ: colon; Vector: pcMV-SPORT6; Site_1:
/Inote="Organ: colon; Vector: pcMV-SPORT6; Site_1:
/Inote="Organ: colon; Vector: pcMV-SPORT6; Site_1:
/Inote="IMAGE:4989195"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGGTGCCTGCGTTCGGGAGAACAACTCTTCCCGCTGGGTAGCGCTCACCCC 380
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CCCTAGCGCCTCCGCCCCCGGCCCCTATCCTCTCTTCCTGCTCTGTCCCTACTTCTC
                        CATGTCGTCGTGCGCCGGGAGCCACCGCCCTCCGGAGACAGGGCAGCTCCCCTACGA 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
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aa26b11.rl NCI_CGAP_GCB1
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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                                                                                                           Conservative
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                                                                                                                                                                      /clone="IMAGE:814365"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GDB:6032522"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
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Primates;
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                       GGGTGCTGCCAGAGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAACTATG 142
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                                                                              CTTCAAGTGCAACAGCGCCGTCTGGAAGGCGCTCAGGGCGGTCGACGCCGTCGCCGTCGG 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCTATGTACGTGGGGGATCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCACCAT 527
                                                                                                                                                                      69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center For Genetic Resource Information National Institute of Genetics
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Unpublished (2002)
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1 (bases 1 to 359)
Ogihara, Y. and Murai, K.
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Location/Qualifiers
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//Ote-stayer recks scale 10.3.4
//Ote-stayer recks scale 10.3.4
//Ote-stayer vector: Lambda Uni_ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a CDNA
library was made, and the CDNA clones were in vivo
excised to give paluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin,
Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
70 a 115 c 107 g 67 t
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Y. Ogihara unpublished cDNA library, Wh_f Triticum
cDNA clone whf25g19 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_11b="Y. Ogihara unpublished cDNA library, Wh_f"/tissue_type="spike at flowering date"/dev_stage="Feekes' scale 10.5.1"
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/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                              GGACGCCGGCAGCCCTGGGCGCAGGACGTCGTGCTGCCGGTGCACGTGCCCAAGG
                                                                                                                                                                                                                                                                                                                                                    GGGTGCTGCCAGAGCCCTGGCGCATGGCGTTCCGGGTTCTGGAAGACGGCGTGAACTATG 142
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                               Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                           AV638521 399 bp mRNA linear EST AV638521 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas cDNA clone HC087d07_r 5', mRNA sequence.

AV638521
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Ogihara, Y. and Murai, K.
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                     Chlamydomonadaceae; Chlamydomonas
                                                                                                                          AV638521.1 GI:10781841
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Y Oglhara unpublished cDNA library, Wh_f"
/tissue_type="spike at flowering date"
/dev_stage="Feekes' scale 10.5.1"
/note="Yector: Lambda Uni-ZAP XR, excised phagemid;
/fite_library Site_1: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                           AV637507 Chlamydomonas reinhardtii 5% CO2
CDNA Clone HC074a01_r 5', mRNA sequence.
AV637507
AV637507.1 GI:10780827
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Generation of expressed sequence tags from adapted cells of Chlamydomonas reinhardtii DNA Res. 7 (5), 305-307 (2000)
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Generation of expressed sequence tags from adapted cells of Chlamydomonas reinhardtii DNA Res. 7 (5), 305-307 (2000)
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1 (bases 1 to 434)
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                                                                                                                                             Contact: Erika Asamizu
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                                 1532-3, Kisarazu, Chiba 292-0812, Japan
l: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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/clone="HC087d07_r"
/clone="Chlamydomonas reinhardtii 5% CO2"
/clone="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescriptII sk-; Site_1 EcoRI; Site_2:
/note="Vector: pBluescriptII sk-; Site_1 EcoRI; Site_2:
in a medium with bubbling air containing 5% carbon
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/organism="Chlamydomonas reinhardtii"
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l Similarity 50.88;
92; Conservative
                                                                                                                                                                                                                                                                                    Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
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                                                                                                                                                                                                       sa DNA Research Institute
1532-3, Kisarazu, Chiba 292-0812, Japan
1: asamizu@kazusa.or.jp, URL:http://www.kazusa.
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/clone_lib="chlamydomonas reinhardtii 5% CO2"
/clone_tib="chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Si
XhoI; The cDNA library was constructed from cells c
in a medium with bubbling air containing 5% carbon
                                                                                  /clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultur.
in a medium with bubbling air containing 5% carbon
                                                                                                                                       /db_xref="taxon:3055"
/clone="HC080c04_r"
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/strain="C9"
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    CATGGGCATCTACGGTCCCCGCACCGTGTTCTGCATTGCCCTGAAGGACGCCCCCGGCTG
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Chlamydomonadaceae, Chlamydomonas.
1 (bases 1 to 450)
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Contact: Erika Asamizu
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l: asamizu@kazusa.or.jp, URL:http:
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                                                                    AV637643 AV637643 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii CDNA clone HC075g03_r 5', mrna sequence.
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/strain="C9"
/db_xref="taxon:3055"
/clone="HC071f12_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
                                            GI:10780963
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AV634724 AV634724 GI:10778044

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                            Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                 Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from adapted cells of Chlamydomonas reinhardtii DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 453)
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1 (bases 1 to 451)
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; S
XhoI; The cDNA library was constructed from cells
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                              Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Chlamydomonas reinhardtii
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Contact: Erika Asamizu
Contact: Aboratory for Plant Gene Research
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
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                                                                      /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
                                                                                                                                         /organism="Chlamydomonas reinhardtii
/strain="C9"
                                                                                               /clone="HC068a04_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
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183 CTTGGCTTTACTGTCCTGTCTGACCATTCCAGCTTCCGCTTATGAGGTGCGCAACGTGTC
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CGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTATGAGGCAGCGGA 302
                                       CTTCGACCCCCTGGACGGCTCGTCCATCGTCGACACCTTCGCCGTGGGCACCATCTT 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV635382 AV635382 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas cDNA clone HC045f10_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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                                                                                                                       Conservative
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                                                                                                                                                                                                                                      /clone="HC045f10_r"
/clone_lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells culture
in a medium with bubbling air containing 5% carbon
dioxide"
                                                                                                                                                                                                                                                                                                                                                                                   /organism="Chlamydomonas
/strain="C9"
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reinhardtii
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Db 341 CATGGGCATCTACGGTCCCCGCACCGTGTTCTGCATTGCCCTGAAGGACGCCCCGGCTG 400

Qy 363 C 363

Db 401 C 401

Search completed: February 18, 2003, 07:07:42

Job time: 1698 secs
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